



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143686

To: Ruixiang Li
Location: rem/4d75/4c70
Art Unit: 1646
Wednesday, February 02, 2005

Case Serial Number: 09/881736

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

This Page Blank (uspto)

STIC-Biotech/ChemLib

CRFE

143686

me

From: Li, Ruixiang
Sent: Sunday, January 30, 2005 2:41 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.09/881,736

78733

Please do a standard search on:

SEQ ID NO: 2 against commercial amino acid databases.

QA-632

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

me

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____
Searcher: Beverly e 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
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Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGN

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:13:02 ; Search time 146 Seconds
(without alignments)
1563.938 Million cell updates/sec

Title: US-09-881-736a-2

Perfect score: 3243

Sequence: 1 MDTMMLNVLNLFQOLVRVE.....SKSATNIGRQGNFFASPMUK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*

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3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*

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20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	9	US-09-881-736-2
2	3230	99.6	632	9	US-09-833-790-413
3	2919	90.0	570	9	US-09-833-790-427
4	2734	84.3	628	9	US-09-881-736-4
5	1182	36.4	255	16	US-10-408-765A-1045
6	541.5	16.7	681	9	US-09-881-736-6
7	334	10.3	2022	16	US-10-408-765A-598
8	322	9.9	175	15	US-10-072-012-878
9	322	9.6	175	15	US-10-072-012-879
10	310	9.6	1261	15	US-10-072-012-733
11	301	9.3	1261	14	US-10-177-980-2
12	301	9.3	1261	16	US-10-648-593-192
13	294.5	9.1	193	9	US-09-802-127-8

14	294	9.1	295	14	US-10-205-194-95	Sequence 95, App1
15	286.5	8.8	718	13	US-10-087-192-333	Sequence 333, App
16	286.5	8.8	1173	15	US-10-072-012-725	Sequence 725, App
17	286.5	8.8	1286	14	US-10-153-668-212	Sequence 212, App
18	286.5	8.8	1286	15	US-10-072-012-724	Sequence 724, App
19	286.5	8.8	1354	14	US-10-153-668-470	Sequence 470, App
20	286.5	8.8	1958	17	US-10-483-506-19	Sequence 19, App1
21	285.5	8.8	996	15	US-10-072-012-731	Sequence 731, App
22	285.5	8.8	1136	15	US-10-072-012-729	Sequence 729, App
23	285.5	8.8	1165	15	US-10-072-012-730	Sequence 730, App
24	285.5	8.8	1192	14	US-10-369-493-3502	Sequence 3502, Ap
25	284.5	8.8	1136	15	US-10-072-012-280	Sequence 280, App
26	284	8.8	1355	15	US-10-072-012-278	Sequence 278, App
27	275.5	8.3	1271	14	US-10-193-651-21	Sequence 21, App1
28	270.5	8.3	2548	9	US-09-851-682A-1	Sequence 1, App1
29	269.5	8.3	735	15	US-10-072-012-726	Sequence 726, App
30	269	8.3	615	13	US-10-087-192-336	Sequence 336, App
31	266.5	8.2	523	15	US-10-072-012-732	Sequence 732, App
32	263.5	8.1	555	9	US-09-764-868-878	Sequence 878, App
33	260.5	8.0	802	17	US-10-684-422-246	Sequence 246, App
34	258	8.0	903	16	US-10-408-765A-827	Sequence 827, App
35	256.5	7.9	659	16	US-10-363-829-303	Sequence 303, App
36	256.5	7.9	707	15	US-10-112-944-256	Sequence 256, App
37	255.5	7.9	1176	14	US-10-032-585-7782	Sequence 7782, Ap
38	255	7.9	569	14	US-10-094-749-1841	Sequence 1841, Ap
39	254.5	7.8	748	14	US-10-104-047-2336	Sequence 2336, Ap
40	253.5	7.8	1846	14	US-10-369-493-4974	Sequence 4974, Ap
41	251	7.7	170	9	US-09-802-127-7	Sequence 7, App1
42	251	7.7	170	13	US-10-080-960-32	Sequence 32, App1
43	247.5	7.6	291	9	US-09-764-868-898	Sequence 898, App
44	247.5	7.6	617	15	US-10-108-260A-4817	Sequence 4817, Ap
45	247	7.6	816	14	US-10-104-047-2328	Sequence 2328, Ap

ALIGNMENTS

RESULT 1

US-09-881-736-2

Sequence 2, Application US/09881736

Patent No. US20020076785A1

GENERAL INFORMATION:

APPLICANT: Glotzer, Michael

APPLICANT: Jantsch-Plunger, Verena

APPLICANT: Romano, Alper

APPLICANT: Mishima, Masanori

APPLICANT: Kaitna, Susanne

TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in

FILE REFERENCE: 0652.2260001/EKS/AES

CURRENT APPLICATION NUMBER: US/09/881, 736

CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: EP 00 112 880.0

PRIOR FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: EP 01 110 554.1

PRIOR FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/241,231

PRIOR FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: To be determined

PRIOR FILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 632

TYPE: PRT

ORGANISM: Homo sapiens

US-09-881-736-2

Query Match 100.0%; Score 3243; DB 9; Length 632;

Best Local Similarity 100.0%; Pred. No. 8.2e-258;

Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDTMMLNVLNLFQOLVRVEIISGNEVOFIQLAKDFEDFRKKKORTDHELKYLMLMK 60

Db 1 MDTMMLNVNLFEOQLVRRVEIISSENEVFIQLAKDFEDFRKKWQRTDHELKCYKDLNKK 60
Qy 61 ATERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
Db 61 ATERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
Qy 121 QKSALAFLNRGQSSSNAKNKRLSTIDESGSIISDIPKTBESLDWDSLVKTFKLKR 180
Db 121 QKSALAFLNRGQSSSNAKNKRLSTIDESGSIISDIPKTBESLDWDSLVKTFKLKR 180
Qy 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQNESIVAKTIVVPNDGPIEAVSTIETVP 240
Db 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQNESIVAKTIVVPNDGPIEAVSTIETVP 240
Qy 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTIVIKPESC 300
Db 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTIVIKPESC 300
Qy 301 VPCGKRIRKFKLSLKCRCRQVSHPECRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB 360
Db 301 VPCGKRIRKFKLSLKCRCRQVSHPECRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB 360
Qy 361 MIPSTIVHCVNIEQRLTETGLYRISGCDRTVKEKEKFLKRVKTVPLSKVDIHAICS 420
Db 361 MIPSTIVHCVNIEQRLTETGLYRISGCDRTVKEKEKFLKRVKTVPLSKVDIHAICS 420
Qy 421 LKQDFLRNKEPLTLFRLNRAFMEAAEITDEDNSIAAMYQAVGELPOANRDLTAFIMIH 480
Db 421 LKQDFLRNKEPLTLFRLNRAFMEAAEITDEDNSIAAMYQAVGELPOANRDLTAFIMIH 480
Qy 481 QVVAOSPHTKMDVANIAXYFGPTIVAAVNPDPVTMSODIKRQPVVERLLSLPLEYWS 540
Db 481 QVVAOSPHTKMDVANIAXYFGPTIVAAVNPDPVTMSODIKRQPVVERLLSLPLEYWS 540
Qy 541 QPMWMEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLKTSSSSLSQRVNS 600
Db 541 QPMWMEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLKTSSSSLSQRVNS 600
Qy 601 TLTNTTPRFGSKSKSATNLGRQGNFFASPMK 632
Db 601 TLTNTTPRFGSKSKSATNLGRQGNFFASPMK 632

RESULT 2
US-09-833-790-413
; Sequence 413, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tonglong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-413

Query Match 99.6%; Score 3230; DB 9; Length 632;
Best Local Similarity 99.7%; Pred. No. 9,7e-257;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDTMMLNVNLFEOQLVRRVEIISSENEVFIQLAKDFEDFRKKWQRTDHELKCYKDLNKK 60

Db 1 MDTMMLNVNLFEOQLVRRVEIISSENEVFIQLAKDFEDFRKKWQRTDHELKCYKDLNKK 60
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Db 61 ATERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
Qy 121 QKSALAFLNRGQSSSNAKNKRLSTIDESGSIISDIPKTBESLDWDSLVKTFKLKR 180
Db 121 QKSALAFLNRGQSSSNAKNKRLSTIDESGSIISDIPKTBESLDWDSLVKTFKLKR 180
Qy 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQNESIVAKTIVVPNDGPIEAVSTIETVP 240
Db 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQNESIVAKTIVVPNDGPIEAVSTIETVP 240
Qy 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTIVIKPESC 300
Db 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTIVIKPESC 300
Qy 301 VPCGKRIRKFKLSLKCRCRQVSHPECRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB 360
Db 301 VPCGKRIRKFKLSLKCRCRQVSHPECRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB 360
Qy 361 MIPSTIVHCVNIEQRLTETGLYRISGCDRTVKEKEKFLKRVKTVPLSKVDIHAICS 420
Db 361 MIPSTIVHCVNIEQRLTETGLYRISGCDRTVKEKEKFLKRVKTVPLSKVDIHAICS 420
Qy 421 LKQDFLRNKEPLTLFRLNRAFMEAAEITDEDNSIAAMYQAVGELPOANRDLTAFIMIH 480
Db 421 LKQDFLRNKEPLTLFRLNRAFMEAAEITDEDNSIAAMYQAVGELPOANRDLTAFIMIH 480
Qy 481 QVVAOSPHTKMDVANIAXYFGPTIVAAVNPDPVTMSODIKRQPVVERLLSLPLEYWS 540
Db 481 QVVAOSPHTKMDVANIAXYFGPTIVAAVNPDPVTMSODIKRQPVVERLLSLPLEYWS 540
Qy 541 QPMWMEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLKTSSSSLSQRVNS 600
Db 541 QPMWMEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLKTSSSSLSQRVNS 600
Qy 601 TLTNTTPRFGSKSKSATNLGRQGNFFASPMK 632
Db 601 TLTNTTPRFGSKSKSATNLGRQGNFFASPMK 632

RESULT 3
US-09-833-790-427
; Sequence 427, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tonglong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-427

Query Match 90.0%; Score 2919; DB 9; Length 570;
Best Local Similarity 99.8%; Pred. No. 3.4e-231;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 63 TERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQLIREMLMCDTSGSIOLSEBOK 122

Db 1 TERSSALDVKLKHARNOVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQISEQK 60
Qy 123 SALAFINRGQSSSNAGNRLSTIDSGSLSDISPKTDESIDMDSIVTKTKRKREK 182
Db 61- SALAFINRGQSSSNAGNRLSTIDSGSLSDISPKTDESIDMDSIVTKTKRKREK 120
Qy 183 RSTSHQFVDPGPPGPKTKRSIGSAVDQNGESIIVAKTTVTPVNDGPIEAVSTIETVY 242
Db 121 RSTSHQFVDPGPPGPKTKRSIGSAVDQNGESIIVAKTTVTPVNDGPIEAVSTIETVY 180
Qy 243 TRSRRTGTGLQPNNSDSTLNSRQLEPRTETDSVGTQPSNGMRLHDFVSKTVIKPES 302
Db 181 TRSRRTGTGLQPNNSDSTLNSRQLEPRTETDSVGTQPSNGMRLHDFVSKTVIKPES 240
Qy 303 CGRKIRFGKSLKCRQCRVSHPECRCRCPCLPILIGTPVKIGEGMLADPVFSQTS 362
Db 241 CGRKIRFGKSLKCRQCRVSHPECRCRCPCLPILIGTPVKIGEGMLADPVFSQTS 300
Qy 363 PSIVHCVNEIEBQRLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKYDDIHAICSL 422
Db 301 PSIVHCVNEIEBQRLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKYDDIHAICSL 360
Qy 423 KQFLRLNKEBLLTFRLNRAFMEEAETDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 482
Db 361 KQFLRLNKEBLLTFRLNRAFMEEAETDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 420
Qy 483 VQSPHTKQDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERBRLSLPLEYWSOF 542
Db 421 VQSPHTKQDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERBRLSLPLEYWSOF 480
Qy 543 MMEQENIDPLAHYIENSNAFSTPOTPDIKVSLGPTVTPHQLLTPSSSSLSQRYSTL 602
Db 481 MMEQENIDPLAHYIENSNAFSTPOTPDIKVSLGPTVTPHQLLTPSSSSLSQRYSTL 540
Qy 603 TKNTPRFGSKSKSATNLGRQGNFPASPMLK 632
Db 541 TKNTPRFGSKSKSATNLGRQGNFPASPMLK 570

RESULT 4
US-09-881-736-4
; Sequence 4, Application US/09881736
; Patent No. US20020076785A1
; GENERAL INFORMATION:
; APPLICANT: Glotzer, Michael
; APPLICANT: Jantech-Plunger, Verena
; APPLICANT: Romano, Alper
; APPLICANT: Mishima, Masanori
; APPLICANT: Kaitna, Susanne
; TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
; FILE REFERENCE: 0632,2260001/EKS/ABS
; CURRENT APPLICATION NUMBER: US/09/881,736
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: EP 00 112 880.0
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: EP 01 110 554.1
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/241,231
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: To be determined
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-881-736-4

Query Match 84.3%; Score 2734; DB 9; Length 628;
Best Local Similarity 84.4%; Pred. No. 6,7e-216;

Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3;
Qy 1 MOTMNLNENLFEQYLRVVEILSENGE-VQFIQLADPEDFRKKMORTHELCKYDILLM 59
Db 1 MOTMNLNENLFEQYLRVVEILSENGE-VQFIQLADPEDFRKKMORTHELCKYDILLM 60
Qy 60 KAETRSALDVKLKHARNOVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQISE 119
Db 61 KAETRSALDVKLKHARNOVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQISE 120
Qy 120 EOKSALAFINRGQSSSNAGNRLSTIDSGSLSDISPKTDESIDMDSIVTKTKRKREK 179
Db 121 EOKSALAFINRGQSSSNAGNRLSTIDSGSLSDISPKTDESIDMDSIVTKTKRKREK 180
Qy 180 REKRSTSHQFVDPGPPGPKTKRSIGSAVDQNGESIIVAKTTVTPVNDGPIEAVSTIETV 239
Db 181 REKRSTSHQFVDPGPPGPKTKRSIGSAVDQNGESIIVAKTTVTPVNDGPIEAVSTIETV 240
Qy 240 PYWTRSRRTGTGLQPNNSDSTLNSRQLEPRTETDSVGTQPSNGMRLHDFVSKTVIKPES 299
Db 241 PYWTRSRRTGTGLQPNNSDSTLNSRQLEPRTETDSVGTQPSNGMRLHDFVSKTVIKPES 300
Qy 300 CVPCKGRIKFGKSLKCRQCRVSHPECRCRCPCLPILIGTPVKIGEGMLADPVFSQTS 359
Db 301 CVPCKGRIKFGKSLKCRQCRVSHPECRCRCPCLPILIGTPVKIGEGMLADPVFSQTS 360
Qy 360 PMPSIVHCVNEIEBQRLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKYDDIHAIC 419
Db 361 PMPSIVHCVNEIEBQRLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKYDDIHAIC 420
Qy 420 SLIKDFLRLNKEBLLTFRLNRAFMEEAETDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 479
Db 421 SLIKDFLRLNKEBLLTFRLNRAFMEEAETDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 480
Qy 480 LQRAVQSPHTKQDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERBRLSLPLEYWSOF 539
Db 481 LQRAVQSPHTKQDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERBRLSLPLEYWSOF 540
Qy 540 SOPMMEQENIDPLAHYIENSNAFSTPOTPDIKVSLGPTVTPHQLLTPSSSSLSQRYSTL 599
Db 541 SOPMMEQENIDPLAHYIENSNAFSTPOTPDIKVSLGPTVTPHQLLTPSSSSLSQRYSTL 596

RESULT 5
US-10-408-765A-1045
; Sequence 1045, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1045
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1045

Query Match 36.4%; Score 1182; DB 16; Length 255;


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Db      1546 NIKTMSVSPNGKI-----HVGKDLMEVYQIVVSNLATERGQKDTNLVNLFOSTLDEFT 1601
Qy      245 SRRTGTLQPMWNSDSTLNSROLEPRTSDVGTVPQSGMRLLDHFVSKTYIKESGCVPGC 304
Db      1602 GYTK-----NDEPIYKSKAQKKRQKQERAVOENHG---HVFASYQVSIPOSCQCL 1650
Qy      305 KRIKFGKLSKCRDVRVSHPECRDRCPLCIPTL--IGTP-VKIGE-GMLADPVSQTS 360
Db      1651 SYLWMDKALLCGVCKMTCHKKCHKIQSHCSYTGKSGPAGPBGHFGVCDVSLTSDKA 1710
Qy      361 MIRSIVHCVNEIEQRLTGTGLYRISGCRITYKELKEKLRKYKTVPLSKVD--IHAI 418
Db      1711 SVPIVTEKLEHMEVGLYTEGLYKSGAANRTRELFQ---ALQTDPAAYKLENFPHAI 1767
Qy      419 CSLKDFLRNLYKEPLTLFRNRAFMEEAITDENSTIAMYQAVGELPOANRDTLAFMI 478
Db      1768 TGVKQKRLPEPLMTFPAQYGDPLRVLPKQEOALATVAVLEHLPENHNLSLERLIF 1827
Qy      479 HLOQVA-QSPHTMDVANIKAQVGPITVAHAVPNPDPVTMSODIKRQPKVVERLLSLPLE 537
Db      1828 HLKVALLEDVNMSPALAIIFAPCLL-RCPDNSDPLTSMKDYKLTTCVEMLIKQMR 1886
Qy      538 YMSQFMVVEQENIDPLHVIEN-----SNAFSTPQTPD-----IKVSLGAPT 579
Db      1887 KYK-----VKMEISIQLEAAESIAFRRLSLRQVANKSPKTRREPAGAGRLITTSRVP-- 1940
Qy      580 TPEHOLKTPSSSSLSGRVST-----LTKTTPR 608
Db      1941 SPSTRNLALGSMRSALRTGTGRPARPARALRRRPPR 1980
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RESULT 8

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US-10-072-012-878
; Sequence 878, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patuturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
```

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; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 878
; LENGTH: 175
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: GTPase-activator protein for Rho-like GTPases
US-10-072-012-878
```

Query Match 9.9%; Score 322; DB 15; Length 175;
Best Local Similarity 45.1%; Pred. No. 3,7e-18;
Matches 78; Conservative 25; Mismatches 64; Indels 6; Gaps 3;

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Qy      362 IRSIVHCVNEIEQRLTGTGLYRISGCRITYKELKEKLRKYKTVPLLSKVDIHIACSL 421
Db      3 IPIVKEKCLEYKRLDTEGIRKSGASRVVLEAPDSCGDPDLSEYDVHVAAGL 62
Qy      422 LKDFLRNLYKEPLTLFRNRAFMEEAITDENSTIAMYQAVGELPOANRDTLAFMIHIQ 481
Db      63 LKFLRELPEPLITFELYEFTEAKLDEBEERLRRLRELSLPPANRATLRYLLAHNL 122
Qy      482 RVAQ-SPTHMDVANIKAQVGPITVAHAVPNPDPVTMS-ODIKRQPKVVERLL 532
Db      123 RVAHSEBENMTARNLAIVFGPTLR-----PPDGESASLKDIDHOKVVEFLI 171
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RESULT 9

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US-10-072-012-879
; Sequence 879, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patuturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
```

	Query Match	9.9%	Score 322	DB 15	Length 175;	
	Best Local Similarity	45.1%;	Pred.No. 3.7e-18;			
	Matches	78	Conservative	25	Mismatches	64
					Indels	6
					Gaps	3
<hr/>						
Qy	362	IPSIIVHCVNNEIQGLTETGTYLRISGCDRTYKELKEFLRVKYTPLLSKVDIDHAICSL	421			
		: : : : :		:	:	:
Dd	3	IPIIVEKIEIYLEKKGLDTBGTGYRSGSASRYKELREAFDSPPDDLSEFDVADVACL	62			
<hr/>						
Qy	422	LKDPLRLNKPEPLLTERLNRAFMEEAAETDEEDNSIAAMYQAVGELPQANDTLAFTMIHLQ	481			
		: : : : :		:	:	:
Dd	63	LKLFLRELPEPLITELYEELFEAKLDEBEERLALNELLSLPAPARATIRYLALAHNL	122			
<hr/>						
Qy	482	RVAQC-SPTKMDVANLVKFGPTLYAHAVPNDDPYTMG-QDIKRPKYVERILL	532			
		: : : : :		:	:	:
Dd	123	RVASEISEENKTARNIAIVFGEPTLLR---PEDGSASIKDRIHQNKVKVEFPI	171			

```

1  APPLICANT:  Lepley, Denise M.
2  APPLICANT:  Rieger, Daniel K.
3  APPLICANT:  Burgess, Catherine E.
4  TITLE OF INVENTION:  Proteins and Nucleic Acids Encoding Same
5  FILE REFERENCE:  21402-258
6  CURRENT APPLICATION NUMBER:  US//10/072,012

```

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CURRENT FILING DATE: 2002-01-31
PRIORITY APPLICATION NUMBER: 60/265,102
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: 60/265,514
PRIORITY FILING DATE: 2001-01-31
PRIORITY APPLICATION NUMBER: 60/265,517
PRIORITY FILING DATE: 2001-01-31
PRIORITY APPLICATION NUMBER: 60/265,412
PRIORITY FILING DATE: 2001-01-31
PRIORITY APPLICATION NUMBER: 60/265,395
PRIORITY FILING DATE: 2001-01-31
PRIORITY APPLICATION NUMBER: 60/266,406
PRIORITY FILING DATE: 2001-02-02
PRIORITY APPLICATION NUMBER: 60/266,767
PRIORITY FILING DATE: 2001-02-05
PRIORITY APPLICATION NUMBER: 60/267,057
PRIORITY FILING DATE: 2001-02-07
PRIORITY APPLICATION NUMBER: 60/266,975
PRIORITY FILING DATE: 2001-02-07
PRIORITY APPLICATION NUMBER: 60/267,459
PRIORITY FILING DATE: 2001-02-08
Remaining Priority Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1

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[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 13:56:16 : Search time 164 Seconds
(without alignments)
1382.420 Million cell updates/sec

Title: US-09-881-736A-2
Perfect score: 3243
Sequence: 1 MDTMMLNVLNFEQLVRVE.....SKSATNLGRQGNFFASPMLEK 632

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3237	99.8	632	4	ABU53065 Human sig
2	3237	99.8	632	7	ADBE60209 Human pro
3	3237	99.8	632	7	ADPE5165 Human Rac
4	3237	99.8	632	8	ADO20214 Human PRO
5	3233	99.7	632	4	AAM40047 Human pol
6	3230	99.6	632	5	AAM69419 Lung smal
7	2919	90.0	570	5	AAM69422 Lung smal
8	2734	84.3	628	7	ADBE60207 Rat Prote
9	1182	36.4	255	4	AAB94223 Human pro
10	1182	36.4	255	7	ADU59239 Human pro
11	971.5	30.0	256	4	AAM32069 Human hea
12	864	26.6	625	4	ABBE8056 Drosophi
13	625	19.3	4318	4	ABG14787 Novel hum
14	618	19.1	1086	4	ABG10230 Novel hum
15	618	19.1	1086	4	ABG13958 Novel hum
16	581	17.9	119	4	AAM41833 Human pol
17	477	14.7	384	4	ABBS9247 Drosophi
18	334	10.3	2022	7	ADJ68792 Human hea
19	323.5	10.0	1240	6	ABRA1659 Human DIT
20	323.5	10.0	2158	5	ADDI18702 Human dis
21	322	9.9	175	5	ADII17343 Polypepti
22	322	9.9	175	5	ADII17342 Polypepti
23	322	9.9	175	5	ADII17342 Polypepti
24	322	9.9	334	4	AAM39659 Human pol
25	322	9.9	352	4	AAM41445 Human pol

26	322	9.9	476	6	ABR41263 Human DIT
27	310	9.6	1261	5	ADII17197 Human NOV
28	301	9.3	1261	5	AAW75995 GRPase ac
29	301	9.3	1261	3	AAV90268 Human GTP
30	301	9.3	1261	8	ADL61268 Human tyr
31	294.5	9.1	193	4	AA667553 Amino aci
32	294	9.1	295	7	ADAB85214 Rat chima
33	294	9.1	1019	6	ADAI13329 Human int
34	293.5	9.1	466	6	ABR58660 Human can
35	293.5	9.1	468	7	ADBS9897 Human pro
36	290.5	9.0	736	2	AAW7809 Human GTP
37	290.5	9.0	759	4	ABG16793 Novel hum
38	290.5	9.0	800	4	ABG16794 Novel hum
39	290.5	9.0	926	7	ADCG90731 Hepatic s
40	286.5	8.8	856	3	AA841660 Human ORF
41	286.5	8.8	1173	4	AA897911 Human G-P
42	286.5	8.8	1173	5	ADII17189 Human NOV
43	286.5	8.8	1286	5	ADII17188 Human NOV
44	286.5	8.8	1286	7	ADG10622 Human STA
45	286.5	8.8	1354	7	ADG10880 Human STA

ALIGNMENTS

RESULT 1
ABU53065
ID ABU53065 standard; protein; 632 AA.
XX AC ABU53065;
XX DT 14-APR-2003 (first entry)
XX DE Human signal transduction-associated protein from DKFZphtes3_1c1.
XX KW Human; gene therapy; vaccine; disease treatment; detection.
XX OS Homo sapiens.
XX PN W0200112659-A2.
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000MO-IB001496.
XX PR 18-AUG-1999; 99US-0149499P.
XX PR 28-SEP-1999; 99US-0156503P.
XX PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX PI Wiemann S;
XX DR WPI; 2001-327840/34.
XX DR N-PSDB; ABX71357.
XX PT Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
XX PS Claim 21; Page 659; 1095pp; English.
XX CC This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by CC them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate polypeptide expression. The products of the CC invention may also be used to identify modulators of expression and CC activity and to down regulate expression and activity. The antibodies of CC the invention may also be used as diagnostic agents for detecting the CC presence of polypeptides in samples. This sequence represents a CC polypeptide described in the disclosure of the invention
XX SO Sequence 632 AA;

Query Match 99.8%; Score 3237; DB 4; Length 632;
 Best Local Similarity 99.8%; Pred. No. 2.2e-263;
 Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MDTMMLNVNLFQVLRRVEIISSENEVOFIOLAKDFEDPRKKMORTDHELGYKDLNKK 60
   |||||
DB 1 MDTMMLNVNLFQVLRRVEIISSENEVOFIOLAKDFEDPRKKMORTDHELGYKDLNKK 60
QY 61 AETERSALDVKLKHANOVDAEIKRORAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
   |||||
DB 61 AETERSALDVKLKHANOVDAEIKRORAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
QY 121 QKSALAFLNRGQPSNNAGNKRSLSTIDSGSILSDISFPKTBESLDMDSLVYTFKLKRR 180
   |||||
DB 121 QKSALAFLNRGQPSNNAGNKRSLSTIDSGSILSDISFPKTBESLDMDSLVYTFKLKRR 180
QY 181 EKRRSTSRQFVDPGPPVKKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
   |||||
DB 181 EKRRSTSRQFVDPGPPVKKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
QY 241 YWTRSRRTKGTIOPMNSDSTLNSRQLEPRTETDVSVPQSNNGMRLLHDFVSKTVIKPESC 300
   |||||
DB 241 YWTRSRRTKGTIOPMNSDSTLNSRQLEPRTETDVSVPQSNNGMRLLHDFVSKTVIKPESC 300
QY 301 VPCGKRIRFGKSLKCRDCAVSHPECRCRCPICPTIIGTPVKIGEGMLADFVSQTSR 360
   |||||
DB 301 VPCGKRIRFGKSLKCRDCAVSHPECRCRCPICPTIIGTPVKIGEGMLADFVSQTSR 360
QY 361 MIPSIIVHCNVEIEQGLTETGLYRISGCDRTYKELKEKFLRKVTYPLLSKVDIDHAIKS 420
   |||||
DB 361 MIPSIIVHCNVEIEQGLTETGLYRISGCDRTYKELKEKFLRKVTYPLLSKVDIDHAIKS 420
QY 421 LKQDFLRNKEPILFRLNRAFMEEAEITDEDNSIAAMTQAVGELPQANRDLTAFIMIH 480
   |||||
DB 421 LKQDFLRNKEPILFRLNRAFMEEAEITDEDNSIAAMTQAVGELPQANRDLTAFIMIH 480
QY 481 QKVAOSPHTKMDVANAIAKVPGPITVAHAAPNPVTMSQDIKQKQVVERLLSPLEIYNS 540
   |||||
DB 481 QKVAOSPHTKMDVANAIAKVPGPITVAHAAPNPVTMLDIDKQPKVVERLLSPLEIYNS 540
QY 541 QPMVAVQENIDPLHVIENSAFSTPQTPDIKVSILGPVTTPEHQLKTPSSSSLSQRVNS 600
   |||||
DB 541 QPMVAVQENIDPLHVIENSAFSTPQTPDIKVSILGPVTTPEHQLKTPSSSSLSQRVNS 600
QY 601 TLTKNTPRFGSKSKSATNLGRQGNFPASPMLK 632
   |||||
DB 601 TLTKNTPRFGSKSKSATNLGRQGNFPASPMLK 632

```

RESULT 2
 ADE60209
 ID ADE60209 standard; protein; 632 AA.
 XX
 AC ADE60209;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein CAB66728, SEQ ID NO 6115.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SN1; Chung.
 XX
 OS Homo sapiens.
 OS
 PN MO2003016475-A2.
 PN
 PD 27-FEB-2003.
 PD
 PF 14-AUG-2002; 2002WO-US025765.
 PF
 PR 14-AUG-2001; 2001US-0312147P.
 PR
 PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-033347P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR
 DR GENBANK; CAB66728.
 PT
 PT New composition comprising two or more isolated polypeptides, useful for
 preparing a medicament for treating pain in an animal.
 PS
 PS Claim 1, Page; 1017p; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPRO at
 CC ftp.wipro.int/pub/published_pct_sequences.
 XX
 SQ Sequence 632 AA;

Query Match 99.8%; Score 3237; DB 7; Length 632;
 Best Local Similarity 99.8%; Pred. No. 2.2e-263;
 Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MDTMMLNVNLFQVLRRVEIISSENEVOFIOLAKDFEDPRKKMORTDHELGYKDLNKK 60
   |||||
DB 1 MDTMMLNVNLFQVLRRVEIISSENEVOFIOLAKDFEDPRKKMORTDHELGYKDLNKK 60
QY 61 AETERSALDVKLKHANOVDAEIKRORAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
   |||||
DB 61 AETERSALDVKLKHANOVDAEIKRORAEADCEKLEROIQLIREMLMCDTSGSIOLSEB 120
QY 121 QKSALAFLNRGQPSNNAGNKRSLSTIDSGSILSDISFPKTBESLDMDSLVYTFKLKRR 180
   |||||
DB 121 QKSALAFLNRGQPSNNAGNKRSLSTIDSGSILSDISFPKTBESLDMDSLVYTFKLKRR 180
QY 181 EKRRSTSRQFVDPGPPVKKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
   |||||
DB 181 EKRRSTSRQFVDPGPPVKKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
QY 241 YWTRSRRTKGTIOPMNSDSTLNSRQLEPRTETDVSVPQSNNGMRLLHDFVSKTVIKPESC 300
   |||||
DB 241 YWTRSRRTKGTIOPMNSDSTLNSRQLEPRTETDVSVPQSNNGMRLLHDFVSKTVIKPESC 300
QY 301 VPCGKRIRFGKSLKCRDCAVSHPECRCRCPICPTIIGTPVKIGEGMLADFVSQTSR 360
   |||||
DB 301 VPCGKRIRFGKSLKCRDCAVSHPECRCRCPICPTIIGTPVKIGEGMLADFVSQTSR 360

```

QY 361 MIPSIYVHCNVEIQRGLTETGLYRISGCRVTYKELKPKLYKTVPLLSKVDIAHICS 420
 DB 361 MIPSIYVHCNVEIQRGLTETGLYRISGCRVTYKELKPKLYKTVPLLSKVDIAHICS 420
 QY 421 LKQDFLNKLEPLTFLPLNRAFMFAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 DB 421 LKQDFLNKLEPLTFLPLNRAFMFAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 QY 481 QRAVASPHTMDVANIYAKVGPPTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 DB 481 QRAVASPHTMDVANIYAKVGPPTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 QY 541 QPMNVBQENIDPLHVIENSNAFSTPQTPDIKVSILGVTTPHQLKTPSSSSLSQYRS 600
 DB 541 QPMNVBQENIDPLHVIENSNAFSTPQTPDIKVSILGVTTPHQLKTPSSSSLSQYRS 600
 QY 601 TLTKNTPRFGSKSKSATNLRQGNFASPMLK 632
 DB 601 TLTKNTPRFGSKSKSATNLRQGNFASPMLK 632

RESULT 3

ID ADP65165 standard; protein; 632 AA.
 XX ADP65165;
 AC ADP65165;
 DT 12-AUG-2004 (first entry)
 XX

DE Human Rac GTPase activating protein 1, GTPase activating protein.
 XX

KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX

OS Homo sapiens.
 XX

PN W02003072827-A1.
 XX

PD 04-SEP-2003.
 XX

PF 31-OCT-2002; 2002MO-US035433.
 XX

PR 31-OCT-2001; 2001US-0336220P.
 XX

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX

PI Hirsch R, Thornton SL;
 XX

DR WPI, 2003-712740/67.
 XX

DR GENBANK; NP_037409.
 XX

PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 PT

XX Disclosure; Page: 56pp; English.
 XX

CC The invention relates to a novel method for diagnosing and analyzing
 CC autoimmune disease or arthritis. The method comprises obtaining a
 CC patient sample containing mRNA, analyzing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyze the autoimmune disease
 CC or arthritis in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritis, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritis. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX

SQ Sequence 632 AA;

Query Match 99.8%; Score 3237; DB 7; Length 632;
 Best Local Similarity 99.8%; Pred. No. 2.2e-263;
 Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTMMLNVRNLFQOLVRRVETLSEGNVQFIOLAKQPEDRRKKWQRTDHLGKYKDLMK 60
 DB 1 MDTMMLNVRNLFQOLVRRVETLSEGNVQFIOLAKQPEDRRKKWQRTDHLGKYKDLMK 60
 QY 61 AETERSALDYKLAHARQVVEIKRORADCEKLERQIOLIREMLMCTSGSIQUSEE 120
 DB 61 AETERSALDYKLAHARQVVEIKRORADCEKLERQIOLIREMLMCTSGSIQUSEE 120
 QY 121 QKSALAFNRGQSSSNAGNKRLLSTIDSGSILSDISFDXTDESLDWDSSLVTKFKLKR 180
 DB 121 QKSALAFNRGQSSSNAGNKRLLSTIDSGSILSDISFDXTDESLDWDSSLVTKFKLKR 180
 QY 181 EKRRSTSRQVDPDPGQVVKTRISGAVDQNSIYAKTVTVPNDCGPIEAUSTETVP 240
 DB 181 EKRRSTSRQVDPDPGQVVKTRISGAVDQNSIYAKTVTVPNDCGPIEAUSTETVP 240
 QY 241 YMTRSRKKTGTLQPMNSDSTLNSRQLEPRRETSGVTPQSGNGKRLHDFVSKTYIKPESC 300
 DB 241 YMTRSRKKTGTLQPMNSDSTLNSRQLEPRRETSGVTPQSGNGKRLHDFVSKTYIKPESC 300
 QY 301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDCPLPCIPITLLIGTPVKIGEGMLADFVSQTS 360
 DB 301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDCPLPCIPITLLIGTPVKIGEGMLADFVSQTS 360
 QY 361 MIPSIYVHCNVEIQRGLTETGLYRISGCRVTYKELKPKLYKTVPLLSKVDIAHICS 420
 DB 361 MIPSIYVHCNVEIQRGLTETGLYRISGCRVTYKELKPKLYKTVPLLSKVDIAHICS 420
 QY 421 LKQDFLNKLEPLTFLPLNRAFMFAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 DB 421 LKQDFLNKLEPLTFLPLNRAFMFAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 QY 481 QRAVASPHTMDVANIYAKVGPPTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 DB 481 QRAVASPHTMDVANIYAKVGPPTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 QY 541 QPMNVBQENIDPLHVIENSNAFSTPQTPDIKVSILGVTTPHQLKTPSSSSLSQYRS 600
 DB 541 QPMNVBQENIDPLHVIENSNAFSTPQTPDIKVSILGVTTPHQLKTPSSSSLSQYRS 600
 QY 601 TLTKNTPRFGSKSKSATNLRQGNFASPMLK 632
 DB 601 TLTKNTPRFGSKSKSATNLRQGNFASPMLK 632

RESULT 4

ID ADO20214 standard; protein; 632 AA.
 XX ADO20214;
 AC ADO20214;
 XX

DT 12-AUG-2004 (first entry)
 DE Human PRO polypeptide #559.
 XX
 XX Human; PRO: immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR MPI: 2004-420667/39.
 DR N-PSDB; ADO20213.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7, SEQ ID NO 1118, 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 CC
 SQ Sequence 632 AA;
 Query Match 99.8%; Score 3237; DB 8; Length 632;
 Best Local Similarity 99.8%; Pred. No. 2,2e-263;
 Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDTMTLVNLFPEQLVRRVEILSEGNVOFIOLAKDPEDPRKKKORTDHELGKXKDLNKK 60
 DB 1 MDTMTLVNLFPEQLVRRVEILSEGNVOFIOLAKDPEDPRKKKORTDHELGKXKDLNKK 60
 QY 61 AETRSALDVKLGHAHQVDEIKRRQRAEADCEKLEKROLIIREMLMCDTSGSIQLES 120
 DB 61 AETRSALDVKLGHAHQVDEIKRRQRAEADCEKLEKROLIIREMLMCDTSGSIQLES 120
 QY 121 QKSALAFINRGQPSNNAGNKRSLTIDSGSIISDTSFDTBDSLWDSLVVTFKLKR 180
 DB 121 QKSALAFINRGQPSNNAGNKRSLTIDSGSIISDTSFDTBDSLWDSLVVTFKLKR 180
 QY 181 EKRRSTSRQFVDPGPVKKTRISGSAVQGNESIAKTTVVYPNDGPFLEAVSTLETVP 240
 DB 181 EKRRSTSRQFVDPGPVKKTRISGSAVQGNESIAKTTVVYPNDGPFLEAVSTLETVP 240

QY 241 YWTRSRRTGTLPQPNWSDTLNSRQLERTETDVSIGTQSGNGLHDPFVSKTVIKPESC 300
 DB 241 YWTRSRRTGTLPQPNWSDTLNSRQLERTETDVSIGTQSGNGLHDPFVSKTVIKPESC 300
 QY 301 VPCGRIRKFGKSLKCRDPRVVSHEPCRDRCPLPCIPPLIGTPVPIGEGMLDPFSQTS 360
 DB 301 VPCGRIRKFGKSLKCRDPRVVSHEPCRDRCPLPCIPPLIGTPVPIGEGMLDPFSQTS 360
 QY 361 MIPSIIVHGVNEIEORGLTETGLYRISGCDRTVKEKFKLKVTVPLLSKYVDIHAI 420
 DB 361 MIPSIIVHGVNEIEORGLTETGLYRISGCDRTVKEKFKLKVTVPLLSKYVDIHAI 420
 QY 421 LKDFLRNKEPLFLFRNARMEAAETDENSTIAAYQAVGELPQARNDTLAFMLHL 480
 DB 421 LKDFLRNKEPLFLFRNARMEAAETDENSTIAAYQAVGELPQARNDTLAFMLHL 480
 QY 481 QRAVSPHTKMDVANKAVFGPTIYAAHVPNDPVTMSODIKROPVVERLSLPLEYVS 540
 DB 481 QRAVSPHTKMDVANKAVFGPTIYAAHVPNDPVTMSODIKROPVVERLSLPLEYVS 540
 QY 541 QFMVVEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPHQLKTPSSSSLSQ 600
 DB 541 QFMVVEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPHQLKTPSSSSLSQ 600
 QY 601 TLTNTPTPFGSKSKSATNLGRCGNFPASPMLK 632
 DB 601 TLTNTPTPFGSKSKSATNLGRCGNFPASPMLK 632
 RESULT 5
 AAM40047
 ID AAM40047 standard; protein; 632 AA.
 AC AAM40047;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 3192.
 XX
 KW Human; nocrotic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00652191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Dimaac RT;
 XX
 DR MPI: 2001-442253/47.
 DR N-PSDB; AAI59203.
 XX

PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX Example 4; SEQ ID NO 3192; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AA438642-AA442213) with nucleotide,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activation/inhibition activity, chemocytic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 632 AA:

Query Match 99.7%; Score 3233; DB 4; Length 632;
 Best Local Similarity 99.7%; Pred. No. 4.8e-263;
 Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MDTMMLNVNRLFEQVLRVVEILSEGNEVOFIQAKDFEDFRKKMQRTDHELGYKDLMLK 60
 1 MDTMMLNVNRLFEQVLRVVEILSEGNEVOFIQAKDFEDFRKKMQRTDHELGYKDLMLK 60
 61 AETERALDVKLKHANOVDEIKRQRAADCEKLEKROQIOLIREMLMCDTSSIQLSSE 120
 61 AETERALDVKLKHANOVDEIKRQRAADCEKLEKROQIOLIREMLMCDTSSIQLSSE 120
 121 QKSALAFILNRGQSSSNAGNKRLLSTIDESGSIISDISFDKTDLSLMDSSLVKTFKIKKR 180
 121 QKSALAFILNRGQSSSNAGNKRLLSTIDESGSIISDISFDKTDLSLMDSSLVKTFKIKKR 180
 121 QKSALAFILNRGQSSSNAGNKRLLSTIDESGSIISDISFDKTDLSLMDSSLVKTFKIKKR 180
 121 QKSALAFILNRGQSSSNAGNKRLLSTIDESGSIISDISFDKTDLSLMDSSLVKTFKIKKR 180
 181 EKRRTSRROFVDPGPGVKKTRISIGSVNDSISYAKTVVTPNCGPIEAUSTETETP 240
 181 EKRRTSRROFVDPGPGVKKTRISIGSVNDSISYAKTVVTPNCGPIEAUSTETETP 240
 181 EKRRTSRROFVDPGPGVKKTRISIGSVNDSISYAKTVVTPNCGPIEAUSTETETP 240
 181 EKRRTSRROFVDPGPGVKKTRISIGSVNDSISYAKTVVTPNCGPIEAUSTETETP 240
 241 YWTRSRRTKTGLTPMNSDSTLNSRQLEPRTEQSVGTPOSGMRLHDFVSKTVIRPESC 300
 241 YWTRSRRTKTGLTPMNSDSTLNSRQLEPRTEQSVGTPOSGMRLHDFVSKTVIRPESC 300
 241 YWTRSRRTKTGLTPMNSDSTLNSRQLEPRTEQSVGTPOSGMRLHDFVSKTVIRPESC 300
 241 YWTRSRRTKTGLTPMNSDSTLNSRQLEPRTEQSVGTPOSGMRLHDFVSKTVIRPESC 300
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRCRCPICPIPTLLIGTPVKIGEGMLADPVSQTS 360
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRCRCPICPIPTLLIGTPVKIGEGMLADPVSQTS 360
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRCRCPICPIPTLLIGTPVKIGEGMLADPVSQTS 360
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRCRCPICPIPTLLIGTPVKIGEGMLADPVSQTS 360
 361 MIPSIYVHCNLEIENGGLTETGLYRISGCRITYKELKRYKTVPLSKVDIHAFICS 420
 361 MIPSIYVHCNLEIENGGLTETGLYRISGCRITYKELKRYKTVPLSKVDIHAFICS 420
 361 MIPSIYVHCNLEIENGGLTETGLYRISGCRITYKELKRYKTVPLSKVDIHAFICS 420
 361 MIPSIYVHCNLEIENGGLTETGLYRISGCRITYKELKRYKTVPLSKVDIHAFICS 420
 421 LKQDFLNLKEPILTRFLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 421 LKQDFLNLKEPILTRFLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 421 LKQDFLNLKEPILTRFLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 421 LKQDFLNLKEPILTRFLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 481 QRVAGSPHTKMDVANIYKVGPTTVAHAVPNDPVTMSQDIKQPKVVERLLSLPLEYWS 540
 481 QRVAGSPHTKMDVANIYKVGPTTVAHAVPNDPVTMSQDIKQPKVVERLLSLPLEYWS 540
 481 QRVAGSPHTKMDVANIYKVGPTTVAHAVPNDPVTMSQDIKQPKVVERLLSLPLEYWS 540
 481 QRVAGSPHTKMDVANIYKVGPTTVAHAVPNDPVTMSQDIKQPKVVERLLSLPLEYWS 540
 541 QPFMVQENEDPLHVLINENSAFSTPQTPDIKVSILGVTTPHQLKTPSSGSLSORVRS 600
 541 QPFMVQENEDPLHVLINENSAFSTPQTPDIKVSILGVTTPHQLKTPSSGSLSORVRS 600
 541 QPFMVQENEDPLHVLINENSAFSTPQTPDIKVSILGVTTPHQLKTPSSGSLSORVRS 600
 541 QPFMVQENEDPLHVLINENSAFSTPQTPDIKVSILGVTTPHQLKTPSSGSLSORVRS 600
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632

RESULT 6

AAU69419
 ID AAU69419 standard; protein; 632 AA.

XX AAU69419;

DT 30-JAN-2002 (first entry)

DE Lung small cell carcinoma antigen #13.

KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;

OS Homo sapiens.

PN WO200177168-A2.

PD 18-OCT-2001.

PF 11-APR-2001; 2001WO-US011859.

XX 11-APR-2000; 2000US-0196780P.

PR 21-JUN-2000; 2000US-0213361P.

PR 01-SEP-2000; 2000US-0229763P.

PR 05-SEP-2000; 2000US-0230629P.

PR 14-SEP-2000; 2000US-0232565P.

PR 19-DEC-2000; 2000US-0257037P.

PR 08-JAN-2001; 2001US-0260796P.

(CORI-) CORIXA CORP.

XX Lodes MJ, Wang T, Mohamath R, Indirias CY;

DR WPI; 2002-010896/01.

DR N-PSDB; AAS61859.

XX Lung tumor polynucleotide and polypeptides useful in therapy and

PT diagnosis of cancer especially lung cancer.

PS Claim 2; Page 270-271; 295pp; English.

XX The invention relates to novel isolated lung small cell cancer antigen
 CC polynucleotides (I) and polypeptides (II) used in a method of detecting
 CC cancer in a patient. The method is optionally performed by utilising
 CC oligonucleotides (III), where the biological sample from the patient is
 CC contacted with (III), detecting the amount of polynucleotide hybridised
 CC to (III) in the sample and comparing the amount of polynucleotide to a
 CC predetermined cut-off value and thereby determining cancer in a patient.
 CC (I), (II) or antigen-presenting cells expressing (II) is useful for
 CC stimulating and/or expanding T cells specific for a tumour protein. The
 CC method comprises contacting T cells with one of the components under
 CC conditions to permit the stimulation and/or expansion of the cells. A
 CC composition comprising (I) is useful for stimulating an immune response
 CC in a patient and for inhibiting the development of a cancer especially
 CC lung cancer in a patient. An isolated T cell population is useful for
 CC removing tumour cells from the biological sample and for inhibiting the
 CC development of cancer in a patient. AAU69407-AAU69431 represent novel
 CC human lung small cell cancer antigen amino acid sequences of the
 CC invention

XX Sequence 632 AA:

Query Match 99.6%; Score 3230; DB 5; Length 632;
 Best Local Similarity 99.7%; Pred. No. 8.7e-263;
 Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MDTMMLNVNRLFEQVLRVVEILSEGNEVOFIQAKDFEDFRKKMQRTDHELGYKDLMLK 60
 1 MDTMMLNVNRLFEQVLRVVEILSEGNEVOFIQAKDFEDFRKKMQRTDHELGYKDLMLK 60
 61 AETERALDVKLKHANOVDEIKRQRAADCEKLEKROQIOLIREMLMCDTSSIQLSSE 120
 61 AETERALDVKLKHANOVDEIKRQRAADCEKLEKROQIOLIREMLMCDTSSIQLSSE 120
 61 AETERALDVKLKHANOVDEIKRQRAADCEKLEKROQIOLIREMLMCDTSSIQLSSE 120
 61 AETERALDVKLKHANOVDEIKRQRAADCEKLEKROQIOLIREMLMCDTSSIQLSSE 120

```
QY 121 QKSALAFNLRGQSSSSNAGNKKLSTIDESGSLSDISFDPKTDSELDWSSLVYTFKLRK 180
DB 121 QKSALAFNLRGQSSSSNAGNKKLSTIDESGSLSDISFDPKTDSELDWSSLVYTFKLRK 180
QY 181 EKRRETSRQFVGGPPVKKTRSIGAVNOGNESTVAKTTVVPNDGGPIEAVSTIEVP 240
DB 181 EKRRETSRQFVGGPPVKKTRSIGAVNOGNESTVAKTTVVPNDGGPIEAVSTIEVP 240
QY 241 YTRSRKRTGTLOPWNDSSTLNSROLEPRTENDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
DB 241 YTRSRKRTGTLOPWNDSSTLNSROLEPRTENDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
QY 301 VPCGRIRKFGKLSLKCRCRVVSHPECRDRCPICPTPLIGTPVKIGEGMLADFVSQTS 360
DB 301 VPCGRIRKFGKLSLKCRCRVVSHPECRDRCPICPTPLIGTPVKIGEGMLADFVSQTS 360
QY 361 MPTIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKVDIHAICS 420
DB 361 MPTIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKVDIHAICS 420
QY 421 LKDFLRNLKEPLTFRLNRAFMEEAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 480
DB 421 LKDFLRNLKEPLTFRLNRAFMEEAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 480
QY 481 QFVAOSPHTKMDVANLAKVFGPTTVAHAVPNPDVTMSODIKRQFVERLLSLPLEYWS 540
DB 481 QFVAOSPHTKMDVANLAKVFGPTTVAHAVPNPDVTMLQDIKQPKVERLLSLPLEYWS 540
QY 541 QPMWVEQENIDPLHVIENSNASTPOTPDIKVSLGLPVTTPHQLLKTSSSSLSQRVWS 600
DB 541 QPMWVEQENIDPLHVIENSNASTPOTPDIKVSLGLPVTTPHQLLKTSSSSLSQRVWS 600
QY 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
QY 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632

RESULT 7
AAU69422
ID AAU69422 standard; protein; 570 AA.
XX
AC AAU69422;
XX
DT 30-JAN-2002 (first entry)
XX
DE Lung small cell carcinoma antigen #16.
XX
KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
XX
OS Homo sapiens.
XX
PN WO200177168-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US011859.
XX
PR 11-APR-2000; 2000US-0196780P.
PR 21-JUN-2000; 2000US-0213361P.
PR 01-SEP-2000; 2000US-0229763P.
PR 05-SEP-2000; 2000US-0230629P.
PR 14-SEP-2000; 2000US-0232655P.
PR 19-DEC-2000; 2000US-0257037P.
PR 08-JAN-2001; 2001US-0260796P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Lodes MJ, Wang T, Mohamath R, Indrias CY;
XX
XX WPI; 2002-010896/01.
XX
XX N-PSDB; AAS61862.
XX
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```
PT Lung tumor polynucleotide and polypeptides useful in therapy and
PT diagnosis of cancer especially lung cancer.
XX
XX Claim 2; Page 282-284; 295pp; English.
PS
CC The invention relates to novel isolated lung small cell cancer antigen
CC polynucleotides (I) and polypeptides (II) used in a method of detecting
CC cancer in a patient. The method is optionally performed by utilizing
CC oligonucleotides (III), where the biological sample from the patient is
CC contacted with (III), detecting the amount of polynucleotide hybridised
CC to (III) in the sample and comparing the amount of polynucleotide to a
CC predetermined cut-off value and thereby determining cancer in a patient.
CC (I), (II) or antigen-presenting cells expressing (II) is useful for
CC stimulating and/or expanding T cells specific for a tumour protein. The
CC method comprises contacting T cells with one of the components under
CC conditions to permit the stimulation and/or expansion of the cells. A
CC composition comprising (I) is useful for stimulating an immune response
CC in a patient and for inhibiting the development of a cancer especially
CC lung cancer in a patient. An isolated T cell population is useful for
CC removing tumour cells from the biological sample and for inhibiting the
CC development of cancer in a patient. AAU69407-AAU69431 represent novel
CC human lung small cell cancer antigen amino acid sequences of the
CC invention
XX
SQ Sequence 570 AA;
XX
Query Match 90.0%; Score 2919; DB 5; Length 570;
Best Local Similarity 99.8%; Pred. No. 1.2e-236;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 63 TERSALDVKLKIAHQVDEIRROPAEADCKLEBQIOLIRBMLMCTSSGSIQISEBOK 122
DB 1 TERSALDVKLKIAHQVDEIRROPAEADCKLEBQIOLIRBMLMCTSSGSIQISEBOK 60
QY 123 SALAFNLRGQSSSSNAGNKKLSTIDESGSLSDISFDPKTDSELDWSSLVYTFKLRK 182
DB 61 SALAFNLRGQSSSSNAGNKKLSTIDESGSLSDISFDPKTDSELDWSSLVYTFKLRK 120
QY 183 RRTSRQFVGGPPVKKTRSIGAVNOGNESTVAKTTVVPNDGGPIEAVSTIEVP 242
DB 121 RRTSRQFVGGPPVKKTRSIGAVNOGNESTVAKTTVVPNDGGPIEAVSTIEVP 180
QY 243 TTSRRKTGTLQPMWNSDSTLNSROLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 302
DB 181 TTSRRKTGTLQPMWNSDSTLNSROLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 240
QY 303 CGKRIKFGKLSLKCRCRVVSHPECRDRCPICPTPLIGTPVKIGEGMLADFVSQTS 362
DB 241 CGKRIKFGKLSLKCRCRVVSHPECRDRCPICPTPLIGTPVKIGEGMLADFVSQTS 300
QY 363 PSIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKVDIHAICS 422
DB 301 PSIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKVDIHAICS 360
QY 423 KDFLRNLKEPLTFRLNRAFMEEAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 482
DB 361 KDFLRNLKEPLTFRLNRAFMEEAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 420
QY 483 VAQSPHTKMDVANLAKVFGPTTVAHAVPNPDVTMSODIKRQFVERLLSLPLEYWS 542
DB 421 VAQSPHTKMDVANLAKVFGPTTVAHAVPNPDVTMLQDIKQPKVERLLSLPLEYWS 480
QY 543 MWEQENIDPLHVIENSNASTPOTPDIKVSLGLPVTTPHQLLKTSSSSLSQRVSTL 602
DB 481 MWEQENIDPLHVIENSNASTPOTPDIKVSLGLPVTTPHQLLKTSSSSLSQRVSTL 540
QY 603 TKTNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 541 TKTNTPRFGSKSKSATNLGROGNFPASPMLK 570

RESULT 8
ADE60207
```

ID	AD660207 standard; protein; 628 AA.
XX	
AC	ADE60207;
DT	29-JAN-2004 (first entry)
XX	
DE	Rat Protein AAH10715, SEQ ID NO 6113.
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS	Rattus norvegicus.
XX	
PN	WO2003016475-A2.
PD	27-FEB-2003.
PF	14-AUG-2002; 2002MO-US025765.
PR	14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.
PA	(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.
P1	Wolf C, D'urso D, Befort K, Costigan M; MPI; 2003-268312/26. GENBANK; AAH10715.
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PS	Claim 1; Page: 1017pp; English.
CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .
SQ	Sequence 628 AA;
OY	Query Match 84.3%; Score 2734; DB 7; Length 628; Best Local Similarity 84.4%; Pred. No. 5,6e-221; Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3
DB	1 MDMMNLNVRNLEPOLVRRVEILSEGNLVOFTOLANDPEFRKKMORTDHELSKYKDLIM 59 ::: ::: ::: ::: ::: ::: ::: 1 MDTVNVMTLEQLVRRWEIINEGNESLEPIGVAVDFEPRKKRYQTNDLEPKDLL 60

Qy	60	KATTESSALDVLTAKARNOVDVEIKRRQRAEADCEKLERQQLIREMLMCTSSGIQLSE	119
Db	61	KATGSGALDVLTAKARNOVDVEIKRRQRAAECAKLEEQQLIRDLIMCDTSSGIQLSE	120
Qy	120	EOKSALAFINRGQPSSSNAGNRLLSTIDESSILDISIFDKTDESLDMSLSVTEFKLK	179
Db	121	EOKSALAFINRGQASGHAGNNRLSTIDESSILDISIFDKTDESLDMSLSLVNFMFKK	180
Qy	180	REKRRASTSQFVDGPPGPKYKTRISGSVADQGESIYAKTIVTVYVYVNDGPIEAVSTIETV	239
Db	181	REKRRASTSQFIDGPPGPKYKTCISGSVADQANSIYAKTIVTVYVPSGGPIEAVSTIETL	240
Qy	240	PYVTRRRRTKGLTOPNNSDTLNSQLPPTETQSVGTPQSGGRLHDFVSKTIKPEES	299
Db	241	PSVTRRRGKSGPLQPNVNSDSLNSPLPRPTIDTNLGLTPQVTGMRHLHDFVSKTIKPEES	300
Qy	300	CVPCGKRIRKFGKLSLKCRDRCVSHPECRDRCPLPCIPITLLIGTPVKIGEGMLDFVSQTS	359
Db	301	CVPCGKRIRKFGKLSLKCRDRCVSHPECRDRCPLPCIPITLVGTVPKIGEGMLDFVSQAS	360
Qy	360	PMIPSLIVHCVNIEBERGLTEGLYRISGCRITYELKEKRLARKYVPLISKVDDIHAIC	419
Db	361	PMIPALIVHCVNIEBERGLTEGLYRISGCRITYELKEKRLARKYVPLISKVDDIHAIC	420
Qy	420	SLIKDITRLMKEPILTLFRNLRAFMFAEITDEDNISIAAMYQAVGELPOANDTLAFIMIH	479
Db	421	SLIKDITRLMKEPILTLFRNLRAFMFAEITDEDNISIAAMYQAVSELPOANDTLAFIMIH	480
Qy	480	LQFVASSPHTKMDVANLAKVFGPTIVAAHVNPDPVTYSODIKQPFYVERLLSLPLEYV	539
Db	481	LQFVSSQPTDKMDIANLAKVFGPTIVAAHVNPDPVTYFODIKQLKVERLLSLPLEYV	540
Qy	540	SOCPMAYEONINIDPLHVIENSNFSTPPQRPDIKVLISGVTTPBEHQLKTSSSSLSQRYR	599
Db	541	NOCPMAYEONINIDPLHVIENSNFSTPPQRPDIKVLISGVTTPBEHQLKTSSSSLSQRYL	596
Qy	600	STLTKNTPRFSGSKSATYILGRQGNFPASPMLIK 632	
Db	597	N-LSKSTPRFGKSKSATYILGRQGNFPAPYLIK 628	
RESULT 9			
AAB94223			
ID	AAB94223	standard; protein; 255 AA.	
AC	AAB94223;		
XX	26-JUN-2001	(first entry)	
XX	Human protein sequence SEQ ID NO:14587.		
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy.		
XX	Homo sapiens.		
XX	EP1074617-A2.		
XX	07-FEB-2001.		
XX	28-JUL-2000; 2000EP-00116126.		
XX	29-JUL-1999; 99JP-00248036.		
XX	27-AUG-1999; 99JP-00300253.		
XX	11-JAN-2000; 2000JP-00118776.		
XX	02-MAY-2000; 2000JP-00183767.		
XX	09-JUN-2000; 2000JP-00241899.		
XX	(HELI-) HELIX RES INST.		
XX	Oca T, Isegaki T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
XX	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX			

DR MPI; 2001-318749/34.
XX primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
PS Claim 8; SEQ ID NO 14587; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the combination
CC of oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 255 AA;
SQ
Query Match 36.4%; Score 1182; DB 4; Length 255;
Best Local Similarity 99.2%; Pred. No. 8.7e-91;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 397 KEKFLRVKTVPLLSKVDYDIAICSLKDFLRNLKEPLLTFRLNRAFMEEAETITDEDSNIA 456
DB 20 KLFKFLRVKTVPLLSKVDYDIAICSLKDFLRNLKEPLLTFRLNRAFMEEAETITDEDSNIA 79
QY 457 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKDVANLAKVFGPTTVAHVPNDPVT 516
DB 80 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKDVANLAKVFGPTTVAHVPNDPVT 139
QY 517 MSQDIKROPKVERLLSLPLEYWSQPMWEOENIDPLHYIENSNAFSTPQTDPDKVSLG 576
DB 140 MLODIIKROPKVERLLSLPLEYWSQPMWEOENIDPLHYIENSNAFSTPQTDPDKVSLG 199
QY 577 PVTTPHEQLLKTSSSSLSQVRVSTLTNTTPFGSKSKSATNLGROGNFFASPMK 632
DB 200 PVTTPHEQLLKTSSSSLSQVRVSTLTNTTPFGSKSKSATNLGROGNFFASPMK 255
RESULT 10
ADJ69239
ID ADJ69239 standard; protein; 255 AA.
XX
XX ADJ69239;
AC
XX 06-MAY-2004 (first entry)
DE Human heat mitochondrial protein as a therapeutic target Segid1045.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
KM Huntington's disease; osteoarthritis;
KM Leber's hereditary optic neuropathy; LHON;
KM mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KM myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KM neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KM osteopathic; ophthalmological; cytostatic.
XX

OS Homo sapiens.
XX
XX WO2003087768-A2.
XX
XX 23-OCT-2003.
PD
XX
XX 04-APR-2003; 2003WO-US010870.
PF
XX
XX 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
PI
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
XX MPI; 2003-845369/78.
DR
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function.
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 1045; 180pp; English.
PS
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
XX Sequence 255 AA;
SQ
Query Match 36.4%; Score 1182; DB 7; Length 255;
Best Local Similarity 99.2%; Pred. No. 8.7e-91;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 397 KEKFLRVKTVPLLSKVDYDIAICSLKDFLRNLKEPLLTFRLNRAFMEEAETITDEDSNIA 456
DB 20 KLFKFLRVKTVPLLSKVDYDIAICSLKDFLRNLKEPLLTFRLNRAFMEEAETITDEDSNIA 79
QY 457 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKDVANLAKVFGPTTVAHVPNDPVT 516
DB 80 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKDVANLAKVFGPTTVAHVPNDPVT 139
QY 517 MSQDIKROPKVERLLSLPLEYWSQPMWEOENIDPLHYIENSNAFSTPQTDPDKVSLG 576
DB 140 MLODIIKROPKVERLLSLPLEYWSQPMWEOENIDPLHYIENSNAFSTPQTDPDKVSLG 199
QY 577 PVTTPHEQLLKTSSSSLSQVRVSTLTNTTPFGSKSKSATNLGROGNFFASPMK 632
DB 200 PVTTPHEQLLKTSSSSLSQVRVSTLTNTTPFGSKSKSATNLGROGNFFASPMK 255
RESULT 11
AAU32069
ID AAU32069 standard; protein; 256 AA.
XX
XX AAU32069;
AC
XX 18-DEC-2001 (first entry)
DT

XX DE Novel human secreted protein #2560.
 XX XX
 XX Human: vaccination; gene therapy; nutritional supplement;
 XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX OS Homo sapiens.
 XX PN MO200179449-A2.
 XX PD 25-OCT-2001.
 XX PF 16-APR-2001; 2001WO-US008656.
 XX PR 18-APR-2000; 2000US-00552929.
 XX PR 26-JUN-2001; 2001US-00770160.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX PT WPI; 2001-611725/70.
 XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX vaccination, testing and therapy.
 XX PS Claim 20; Page 551; 765pp; English.
 XX CC The invention relates to novel human secreted polypeptides. The
 XX CC polypeptides and antibodies to the polypeptides are useful for
 XX CC determining the presence of or predisposition to a disease associated
 XX CC with altered levels of polypeptide. The polypeptides are also useful for
 XX CC identifying agents (agonists and antagonists) that bind to them. Cells
 XX CC expressing the proteins are useful for identifying a therapeutic agent
 XX CC for use in treatment of a pathology related to aberrant expression or
 XX CC physiological interactions of the polypeptide. Vectors comprising the
 XX CC nucleic acids encoding the polypeptides and cells genetically engineered
 XX CC to express them are also useful for producing the proteins. The proteins
 XX CC are useful in genetic vaccination, testing and therapy, and can be used
 XX CC as nutritional supplements. They may be used to increase stem cell
 XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
 XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 XX CC AAU2510-AAU3304 represent the amino acid sequences of novel human
 XX CC secreted proteins of the invention
 XX SQ Sequence 256 AA;
 Query Match 30.0%; Score 971.5; DB 4; Length 256;
 Best Local Similarity 84.0%; Pred. No. 4.9e-73;
 Matches 205; Conservative 3; Mismatches 27; Indels 9; Gaps 4;
 QY QTSPTMPSIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLRVKTVPLLSKYDDIH 416
 DB 1 QTSPTMPSIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLRVKTVPLLSKYDDIH 60
 QY 417 AICSLKDLRLNKEPLTLRLNRAFEAAETDEDSNIAAMYQAVGELFOANRDTLAF 476
 DB 61 AICSLKDLRLNKEPLTLRLNRAFEAAETDEDSNIAAMYQAVGELFOANRDTLAF 120
 QY 477 MHLQVVAOSPHTKMVANKVFGPTVAHAPNDPVTMSQDIR-OPKVERLLSLP 535
 DB 121 MHLQVVAOSPHTKMVANKVFGPTVAHAPNDPVTMLQHGQGVQKVERLLSLP 180
 QY 536 L-EYMSQFMWVEOE--NIDPLHVIENSNAFTPTQFDIKV---SLGPTVTPPEHQLK 587
 DB 181 LMEYMFESFMDGEGGTPLPLVINSNMFSTPQFDIAKAVPGGGLCVHTAGAEAIQK 240
 QY 588 TPSS 591
 DB 241 GPPS 244

RESULT 12
 ABB68056
 ID ABB68056 standard; protein; 625 AA.
 XX AC ABB68056;
 XX XX
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 30960.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN MO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL12159.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
 XX PT interactions.
 XX XX
 XX XX Disclosure; SEQ ID NO 30960; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
 XX CC useful in developmental biology and in elucidating cell signalling and
 XX CC cell-cell interactions in higher eukaryotes for the development of
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
 XX CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 XX CC ABB72072). The sequence data for this patent did not form part of the
 XX CC printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 625 AA;
 Query Match 26.6%; Score 864; DB 4; Length 625;
 Best Local Similarity 35.1%; Pred. No. 2.4e-63;
 Matches 228; Conservative 110; Mismatches 225; Indels 86; Gaps 21;
 QY 4 MMLNVAQLFEQLYRVEILSEGN-EVQFQLOKDPEDPKKMQRTDHELQKYDLMKAE 62
 DB 1 MALSLASFDLRLRCMQVLIDGTPEEFRLFLMEQHEKCAGYAETARLONEDKSL 60
 QY 63 TERSALDVLKILARNQVDEIRKQPAEADCEKLEKQIOLIREMLMCDTSGISLSEBK 122
 DB 61 TKMGDEGLFLFARRIIDEIKARQAEHERAMESKINAAVADLHNNR---LNNETR 116
 QY 123 SALAFINRQOPSS---NA--GNKRLSTIBESGSLIDISFDKT-DSLDMDSLVKT 174
 DB 117 DKLAFLHT-LPSRRKKSINAVREKSYGDINSTGSLISLDSITISEDDFLD-----VRT 170
 QY 175 FLKKREKRSRSTRQV-----DGPQPVKTR--SIGSAVD----- 209
 DB 171 SK-SMREHRLPLKQOIPVGNKRSRLSTGLNGNSGTTPTTGKSRSSVGIGVEQHTVD 229
 QY 210 --QGNESIVAKTTVTPNDG-GPIEAVSTIETVPYVTRSRRTGTLQPMNSDSTLNSRL 266

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Db 230 VGGAFRCATTKVTIPDGGGVIRAEISTIESIPVIAAGNERIGDGLSTPRRSVLKEATA 289
Qy 267 EPRFETDSV-----GTP-OSNGMRLLHDPVSKTVIKPESGCVPGKRIKFGKLSLKR 317
Db 290 PLPLPVNAMAAPHVAVASGTPQLQHRPLMRNHTFSGQKFLRGDNVCVQCKRIKRFAGVLRGR 349
Qy 318 DCRVSHPRCRRCPRLPCLITLIGTP-VKIGECMLADPVSQSPMIPSVIHCVNEIOR 376
Db 350 DCPVRCHIDCRYLLTVSCVPO-TGTPPTTMTGVTDFAPSAIPMIPALIVHCVEIEAR 408
Qy 377 GLTETGLYISGCDRTVKELEKEKFLKVTVPRLSLKVDJHAIQSLKDFLRNKEPLLTF 436
Db 409 GLTEVGLYLLSSERRYKALKEQFLRGKATPHIGNT-DIVVLCCKYKDFLRSLTEPLIFR 467
Qy 437 RLNRFAEAEITDEDSIAAMYQAVGELPQANRDTLAFMLHLOEVAOSPHTKMDVANI 496
Db 468 SQMKPAPANVQNDPTKADMDLVKSVKQLPQANRDTLAFMLHFORIACPPVLMIPDINI 527
Qy 497 AKVFGPTVAHAVPNPDVPTMSODIKRQKRVVERLLSLPLEVMSQPMVQENIDPLHVI 556
Db 528 SLIFGPTIVGYSTPDDQHAIVTEVFTOKQVMKALLEPVSFEWEOYIV-----IDPTR-- 580
Qy 557 ESNNAFSTPQT-----PDIKVSLHGPVTP-----EHQLKTPSSSS 593
Db 581 -----TPATVYIKRVPSNKNLLSLXATPFGKGTIKKKKFGTTPASA 622

RESULT 13
ABG14787
ID ABG14787 standard; protein; 4318 AA.
XX ABG14787;
XX -DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #14778.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSR-) HYSRQ INC.
XX PI Dmanac RT, Liu C, Tang YT.
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS78974.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostic, forensic, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 45146; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
```

```
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG0377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 4318 AA;
XX Query Match 19.3%; Score 625; DB 4; Length 4318;
XX Best Local Similarity 38.8%; Pred. No. 7.6e-42;
XX Matches 167; Conservative 46; Mismatches 85; Indels 132; Gaps 16;
Qy 216 VAKTIVTPNDGPPI-----AVSTLEVPVYTRSR-----RKYGLQ----- 253
Db 3915 IAKSILSQNKAKGGITLPDFKLYKATVTKTWYVQRAVDQWNRGTGSEIMPHIYNVL 3974
Qy 254 -----PMSDSTLNS-----ROLE-----PRFETDS-----VG 276
Db 3975 IFDKPDKKQWGDLSFNKMCWENWLAICRKLKLPFLTPYTKINSRWIKDLHVRPKTIK 4034
Qy 277 TPQSGMRLLH-----PFSKTVIKPESGCVPGKRIKFGKLSLKRCDRVVSHPCRDR 330
Db 4035 TLEENLGNITQYIGMGKDFMSTK---PKAMAKAIKDKDLIKLSFFC----- 4080
Qy 331 CRLPCIPTLIGTPVXIG-----EGMLADPVSQTSPIPSIVHCVNEIEQ----- 375
Db 4081 -----TAKETIRVNOQPTWEMEKIPATYSDD-----KGLISRYNELKQYKKKKTNP 4128
Qy 376 -----RGLTETGLY-----RISGCDR--TVKSLKER-FLRVTVPL----- 409
Db 4129 IKKWTNDMNRHRSKBDIVAAKKMKCSSLPAIRMOQIKTRMYHLTPRALIIKSGNN 4188
Qy 410 SKVDDIHAIQSLKQFLRNLEKEPLTPRLNRAFEAEITDEDSIAAMYQAVGELPQAN 469
Db 4189 SKYDDIHAIQSLKQFLRNLEKEPLTPRLNRAFEAEITDEDSISAMYQAVGELPQAN 4248
Qy 470 RDTLAFMLHLOEVAOSPHTKMDVANIKAVFEGPTVAHAVPNPDVPTMSODIKRQPKYVE 529
Db 4249 RDTIVFIMHLOEVAOSPHTKMDVANIKAVFEGPTVAHAVPNPDVPTMSODIKRQPKYVE 4308
Qy 530 RLISPLEIYW 539
Db 4309 RLISPLEIYW 4318

RESULT 14
ABG10230
ID ABG10230 standard; protein; 665 AA.
XX ABG10230;
XX AC ABG10230;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #10221.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
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XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX MPI; 2001-639362/73.
XX N-PSDB; AAS74417.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 40589; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 665 AA;
XX
XX Query Match 19.1%; Score 618; DB 4; Length 665;
XX Best Local Similarity 46.9%; Pred. No. 1.4e-42;
XX Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;
XX
XX 255 WNSDSTLNSRQLEPRRTSDSVGTPOSGKRLHDPFSKTVIRPESCVPGCKRIKFGKLSL 314
XX DB WIKD--LNVRPRTIKTLENTLGNITDIDMG-KDFMSKT--PKMATKTKIDKMDLIOL 422
XX 315 KCRDCRVSHPECRDRCPLPCITLIGTPVKIG-----EGMLADPVSQTSPIPIVNH 368
XX QY KSEFFC-----TAKETTRVNRQPTWEKIFATYSSD-----KGLISR 459
XX DB CNEIEQ-----RGLTETGLY---RISGCDR--TVKELKEK-FLRV 403
XX QY 369 CNEIEQ-----RGLTETGLY---RISGCDR--TVKELKEK-FLRV 403
XX DB 460 IYVELKQIYKKKTNNPDKKWTNDMNRHFSKEDIYAAKKHKKSSSLPAIREMDIKTMYR 519
XX QY 404 KTVVPL-----SKYDDIHAISGLKDFLNLKEPLTLRLNRAFMEEAITDEDN 453
XX DB 520 HLTFRVIAIIRKSGNNSKYDDIHAIISLKDPLRNFSEPLTLRLNKAFFEEAIEITDEDN 579
XX QY 454 SIAMVQAVGELQOANRDTLAFIMHLORYAOSPHRTMDVANAIAKFGPTIVAAVNPDP 513
XX DB 580 SISAMQAVGELQOANRDTLVFMHILORVAOSPYTKMNVANLAEVFGSTIVAAVNPDE 639
XX QY 514 PVTMSQDIKQRPVVERLSLPLEYW 539
XX DB 640 PVTMLQDIKQKPVVERLSLPLEYW 665
XX
XX RESULT 15
XX ABG19904

```

```

ID ABG19904 standard; protein, 1086 AA.
XX
XX AC ABG19904;
XX
XX 18-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #19895.
XX
XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX MPI; 2001-639362/73.
XX N-PSDB; AAS84091.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 50263; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1086 AA;
XX
XX Query Match 19.1%; Score 618; DB 4; Length 1086;
XX Best Local Similarity 46.9%; Pred. No. 3.2e-42;
XX Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;
XX
XX 255 WNSDSTLNSRQLEPRRTSDSVGTPOSGKRLHDPFSKTVIRPESCVPGCKRIKFGKLSL 314
XX DB WIKD--LNVRPRTIKTLENTLGNITDIDMG-KDFMSKT--PKMATKTKIDKMDLIOL 843
XX QY 315 KCRDCRVSHPECRDRCPLPCITLIGTPVKIG-----EGMLADPVSQTSPIPIVNH 368
XX DB 844 KSEFFC-----TAKETTRVNRQPTWEKIFATYSSD-----KGLISR 880
XX QY 369 CNEIEQ-----RGLTETGLY---RISGCDR--TVKELKEK-FLRV 403
XX
XX RESULT 15
XX ABG19904

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:08:37 ; Search time 43 Seconds
(without alignments)
1414.163 Million cell updates/sec

Title: US-09-881-736a-2

Perfect score: 3243
Sequence: 1 MDTMMLNVLNLFQOLVRVE.....SKSATNLGRQGNFASPMUK 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	2 D59430	Rac GTPase activat
2	547.5	16.9	681	2 T23454	hypothetical prote
3	477	14.7	383	2 B48122	GTPase-activating
4	477	14.7	384	2 A48122	GTPase-activating
5	348	10.7	1980	2 S54307	myosin heavy chain
6	334	10.3	2022	2 A59256	myosin-Ixb [simila
7	329	10.1	334	2 S29128	N-chimerin - rat
8	322	9.9	289	2 S08242	N-chimerin - human
9	320	9.9	239	2 A43953	Gem-interacting pr
10	308	9.5	695	2 T39954	probable gtpase ac
11	301	9.3	1261	2 E59430	PTPL1-associated R
12	294	9.1	295	2 S29956	beta-chimerin - ra
13	294	9.1	443	2 B53764	beta-chimerin, ce
14	293.5	9.1	466	2 A53764	beta-chimerin, ce
15	291	9.0	970	2 D59435	Gem-interacting pr
16	290.5	9.0	814	2 F59430	GTPase regulator a
17	286.5	8.8	1944	2 A59438	KIAA1424 protein l
18	285.5	8.8	1165	2 D59433	C. elegans protein
19	282	8.7	859	2 A49307	98k GTPase-activat
20	281	8.7	822	2 B47485	ABR protein 2 - hu
21	280	8.7	822	2 A47485	ABR protein 1 - hu
22	280.5	8.6	733	2 S44876	CC21.4 protein - C
23	275.5	8.5	1271	1 TVHUBR	hypothetical prote
24	270.5	8.3	1397	2 T46354	hypothetical prote
25	270.5	8.3	2548	2 E59435	myosin IXA (import
26	269.5	8.3	735	2 A59434	KIAA1501 protein l
27	267.5	8.2	2626	2 T31099	myosin-Rhocap prot
28	260.5	8.0	802	2 H59434	oligophrenin 1, Rh
29	258	8.0	903	2 T00705	N-chimerin homolog

30	253.5	7.8	1846	2 T33079	hypothetical prote
31	247.5	7.6	655	2 A59430	hypothetical prote
32	247	7.6	863	2 T27958	hypothetical prote
33	245	7.6	1445	2 A59437	KIAA1204 protein l
34	240	7.4	969	2 T36478	Rhocap/LIM domain
35	238	7.3	974	2 E59434	Rho GTPase activat
36	232	7.2	666	2 S29349	hypothetical prote
37	231.5	7.1	647	2 A57467	RalBP1 - rat
38	231	7.1	818	2 A59433	KIAA0672 protein l
39	229.5	7.1	574	2 T29005	hypothetical prote
40	229.5	7.1	655	2 E59435	rala-binding prote
41	229	7.1	634	2 T27959	hypothetical prote
42	228.5	7.0	837	2 T19825	hypothetical prote
43	222.5	6.9	892	2 T40040	GTPase-activator p
44	221.5	6.8	316	2 T46471	hypothetical prote
45	217	6.7	512	2 E59437	F02569_2 protein l

ALIGNMENTS

RESULT 1

D59430
Rac GTPase activating protein 1 [imported] - human
C/Species: Homo sapiens (man)
C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #ext_change 09-Jul-2004
C/Accession: D59430
R/Kawashima, T.; Kitamura, T.; Nosaka, T.; Hirose, K.
Submitted to Genbank, December 1999
A/Description: Homo sapiens Rac GTPase activating protein 1 (RACGAP1), mRNA.
A/Reference number: D59430
A/Accession: D59430
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-632 <KAM>
A/Cross-references: UNIPROT:Q9P2M2; GB:NP_037409; PIR:g7019433; PIR:NP_037409.1

Query Match	Best Local Similarity	Score	Pred. No.	Length	Matches	Conservative	Mismatches	Indels	Gaps
100.0%;	100.0%;	3243;	DB 2;	632;	632;	0;	0;	0;	0;
1	MDTMMLNVLNLFQOLVRVEIIISGNEVOFIQAKDFEDFRKKWORTDHELKYYKDLMMK 60								
1	MDTMMLNVLNLFQOLVRVEIIISGNEVOFIQAKDFEDFRKKWORTDHELKYYKDLMMK 60								
61	AETERSALDVKUKHARNQDVVEIKRORABADEKLERQIOLIREMLMCDTSGSIQSE 120								
61	AETERSALDVKUKHARNQDVVEIKRORABADEKLERQIOLIREMLMCDTSGSIQSE 120								
121	OKSALAFNLRGQSSNAGKRLSTIDSGSILSDISPKTDBSLDMSLVTFFLKLR 180								
121	OKSALAFNLRGQSSNAGKRLSTIDSGSILSDISPKTDBSLDMSLVTFFLKLR 180								
121	OKSALAFNLRGQSSNAGKRLSTIDSGSILSDISPKTDBSLDMSLVTFFLKLR 180								
181	EKRRTSRQFVDPGPGPVKKTRISGAVDQNESIVAKTTVVVPNDGPIBAVSTIEVP 240								
181	EKRRTSRQFVDPGPGPVKKTRISGAVDQNESIVAKTTVVVPNDGPIBAVSTIEVP 240								
181	EKRRTSRQFVDPGPGPVKKTRISGAVDQNESIVAKTTVVVPNDGPIBAVSTIEVP 240								
241	YMTSRRTKGTLOPMNSDSTLNSROLEPRTEDSVCTPOSGMRLHDPFSKVIRPESC 300								
241	YMTSRRTKGTLOPMNSDSTLNSROLEPRTEDSVCTPOSGMRLHDPFSKVIRPESC 300								
241	YMTSRRTKGTLOPMNSDSTLNSROLEPRTEDSVCTPOSGMRLHDPFSKVIRPESC 300								
301	VPCGRKIKFGKLSLKCRDRCVSHPECRDRCPLPCLITLIGTPVKIGEGMLADVFQSTSP 360								
301	VPCGRKIKFGKLSLKCRDRCVSHPECRDRCPLPCLITLIGTPVKIGEGMLADVFQSTSP 360								
301	VPCGRKIKFGKLSLKCRDRCVSHPECRDRCPLPCLITLIGTPVKIGEGMLADVFQSTSP 360								
361	MPSIVHVCNVEIEQRLTETGLYRISGCDRTYKELKEFLRVKTVPLLSKVDIHAICS 420								
361	MPSIVHVCNVEIEQRLTETGLYRISGCDRTYKELKEFLRVKTVPLLSKVDIHAICS 420								
361	MPSIVHVCNVEIEQRLTETGLYRISGCDRTYKELKEFLRVKTVPLLSKVDIHAICS 420								
421	LKDPFLNKEPLTLFRLNRAFWEAETIDENSIAAMQAVGELPOANRDTLAFIMIH 480								
421	LKDPFLNKEPLTLFRLNRAFWEAETIDENSIAAMQAVGELPOANRDTLAFIMIH 480								
421	LKDPFLNKEPLTLFRLNRAFWEAETIDENSIAAMQAVGELPOANRDTLAFIMIH 480								

```

QY 481 QVAOSPHKMDVANKAKVGPPIVAHAANPNPVTMSQDIKQKRVVERLLSLPEYWS 540
DB 481 QVAOSPHKMDVANKAKVGPPIVAHAANPNPVTMSQDIKQKRVVERLLSLPEYWS 540
QY 541 QPMVAQOEINIDPLHVIENSNAFSTPOTPDIKVSLGPVTPPEHQLKTSSSSLSQRYVS 600
DB 541 QPMVAQOEINIDPLHVIENSNAFSTPOTPDIKVSLGPVTPPEHQLKTSSSSLSQRYVS 600
QY 601 TLTKNTPRFSGSKSATNLGRQGNFPASPMLK 632
DB 601 TLTKNTPRFSGSKSATNLGRQGNFPASPMLK 632

RESULT 2
T23454
hypothetical protein K08E3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23454
R:McMurry, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19743
A:Accession: T23454
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-661 <MIL>
A:Cross-references: UNIPROT:Q9XU99; EMBL:Z81568; PIDN:CA804593.1; GSPDB:GN00021; CESP:K0
A:Experimental source: clone K08E3
C:Genetics:
A:Gene: CESP:K08E3.6
A:Map position: 3
A:introns: 36/1; 73/2; 237/3; 361/3; 612/3

Query Match 16.9%; Score 547.5; DB 2; Length 681;
Best Local Similarity 26.0%; Pred. No. 6.9e-27;
Matches 181; Conservative 109; Mismatches 284; Indels 121; Gaps 22;

QY 7 NVNLFEOIVRRVEIISSENOVOFIQADPFEDFRKM-----ORTDELAGKYDLM 59
DB 14 NSRHIFNMILNSQRPQFDIKDIGMFHLIDEIERLRLKMDSESKRLNADMEAEAL 73
QY 60 KATERSALADVILKARNQVDVEIKRQAEADCELEQIOLIREMLMCDTSGTQISE 119
DB 74 KARKKLAMPDIDVQDKQLRALMEENKALKDLNVEFREKQLKAMKNGIIFNS--LTK 131
QY 120 EOKSALAFINRGOPSSSNAKNKSLTIDSGSILSDISFDKTDSELDMD---SLVYTER 176
DB 132 EDRDQKFLHE---PLVRYYSKRVQ--QRHPLMETDDEDESDVDYETGDSFEVH 186
QY 177 LKK-REKRSTS-----ROFVDGPPG---PVKK 200
DB 187 LANGEVEVRRSSAAGNAVGVKRSASAHATTAANSKRSRSRVMTATIDEEPNEGCTPPKR 246
QY 201 TSSISAVNOGNEISYAKTVT-----VPNDGP-----IEAVSTIEYTP 240
DB 247 CRDDGSTPHQEMTTTTTTTTTTTTTINRAQNDPVPVSLHROLTRRSLSGSIPTSCDQTP 306
QY 241 YVTRSRKKTGTLQPMNSDSTLNSRQLEPRTEPDSVGTPOSSNGMRLHDFVSKTVIKPESC 300
DB 307 GGTNNIGIGMSAIIITKSTLDITLKRGTPRAWTNITR-DIAMRHHTIIEAGIKAMKRC 365
QY 301 VEGKRIKFGKLSLKCRDGRVNSHPRCRCPPLP-----TLIGTPVKIGEGM 350
DB 366 DKCATATKLA-TSMKCRDCHQVNVHRSCKNKLHPCIRPKTMMTPKSALRGAKPAGGEPR 424
QY 351 LADPVSQTSPTMPSIVVHCNVELEQGLTETGLYRISGCDRYKELKEFKRYKTYPLLS 410
DB 425 IODFCTSAKPMI PAAYTHCVVALEAGLTOEGYRPGQVRTVNVILDE-LRSKTYPNVG 483
QY 411 KYDDIHAIQSLKDFLNLKEPILTRLRAPFWEAEI--TDEDNSIAAMYQAVGELPOA 468
DB 484 -LHDEAVITDTLKRFLRDLKDPILPRTSROELIVAAANLSTDPDNGRLALNRVICELPOA 542

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```

QY 469 NDDTLAFMITHIQRV-AQSPHTRMDVANKAKVGPPIVAHAANPNPVTMSQ-----D 520
DB 543 NDDTLAFMITHIQRV-AQSPHTRMDVANKAKVGPPIVAHAANPNPVTMSQ-----D 520
QY 521 IKRQKRVVERLLSLPEYWSQPMVQENIDPLHVIENSNAFSTPOTPD-----IKVSLG 576
DB 597 ATDCHRAMTALFEFDDVYQKFLGISA-----VSMASNOIETARHQNPFALCDRSILG 649
QY 577 PYTTEHQLKTSSSSLSQRYVSTLTKNTPRFSG 611
DB 650 PYTT-----SPATPLARSAANTRARGAHLIGS 677

```

```

RESULT 3
B48122
GTPase-activating protein Rac homolog, splice form clone pcl.7d - fruit fly (Drosophila
C:Species: Drosophila melanogaster
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C:Accession: B48122
R:Aguel, M.; Roder, L.; Vola, C.; Giffin-Shea, R.
Mol. Cell. Biol. 12, 5111-5122, 1992
A>Title: A Drosophila round transcript expressed during spermatogenesis and imaginal di
A:Reference number: A48122; MUID:93024458; PMID:1406685
A:Accession: B48122
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-363 <AGN>
A>Note: sequence extracted from NCBI backbone (NCBIN:115662, NCBI:115663)
C:Genetics:
A:Gene: FlyBase:rn
A:Cross-references: FlyBase:Fbgn0003263

Query Match 14.7%; Score 477; DB 2; Length 383;
Best Local Similarity 40.7%; Pred. No. 8.9e-23;
Matches 110; Conservative 44; Mismatches 102; Indels 14; Gaps 6;

QY 279 QSNCG-MRLHDFVSKT-VIKPESYPCGRIKIFGKLSKCRDGRVNSHPRCRCPPL 336
DB 78 QSHSGILREHNFKISYYNVNVCVHCRKRIRFAMASLRACRCPPLRGCCROLVNCI 137
QY 337 P-TLIGTPVKIGEGMLADPVSQSPMIPSIIVVHCNVELEQGLTETGLYRISGCDRYKE 395
DB 138 PGPQIGTK---RGCLSDAPRVAEPVPAIVACHYTEIEARGLQEGLRVSTTECKR 193
QY 396 LKEKFLRYKTVPLIKVDDIHAICSLKDFLNLKEPILTRLRAPFWEAEITDEDNSI 455
DB 194 LARKLIRKSGSTHIGN-KDTHLCCCVDFLQVLNHLPIYHRDDEEATNHEBRLAYE 252
QY 456 AAMYQAVGELPOANDTLAFMITHIQRVASQSPHTMDVANKAKVGPPIVAHAANPNP 515
DB 253 MAVYLAIVELHQANDDTLALYMLHMOKIAESPAVMTVNNLAVIPAPLFG-----DLD 306
QY 516 TMSQDIKQKRVVERLLSLPEYWSQPMV 545
DB 307 LTLENVVTQKRVLKVLLMPAGFMSQFLEV 336

```

```

RESULT 4
A48122
GTPase-activating protein Rac homolog, splice form clone pcl.7 - fruit fly (Drosophila m
C:Species: Drosophila melanogaster
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48122
R:Aguel, M.; Roder, L.; Vola, C.; Giffin-Shea, R.
Mol. Cell. Biol. 12, 5111-5122, 1992
A>Title: A Drosophila round transcript expressed during spermatogenesis and imaginal di
A:Reference number: A48122; MUID:93024458; PMID:1406685
A:Accession: A48122
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-384 <AGN>
A:Cross-references: UNIPROT:P40809
A>Note: sequence extracted from NCBI backbone (NCBIN:115660, NCBI:115661)

```



```

Qy 71 ----KTKARNVDVEIKRQRAEADCEKLEROIQIREMLMCDISGSIQISEEQKSALA 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1459 PEGOOHRHAAAGE-----KRTKEPGGKGKKNNRVKI-----GKITVEKMESEVF 1502
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 127 FLNRQGPSSNNGKRLSTIDE-SSGILSDISFDKTDSDLDSSLVKTFKLKKREKRS 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1503 ----ROITAN-----ELKYLDEFLNKLINDLSQKTP-----TESLFIENAEKFRS 1545
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 186 TSROFDPGPPGVKTRISGSAVDQGNESIVAKTIVTVNPDDGPLEAVSTIET-VPYWR 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1546 NIKTMYSVANGKI-----HGYVDLMENYQIVVSNLATERGQDQTNVLMFLQSLDEFIR 1601
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 245 SRKKGITLQPMNSDSTLNSRQLEPRTETDSVGTPOSGMGRLHDPVSKTVIKPESCVPG 304
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1602 GYTK-----NDPEFVKOSKQAKKQKQKQRAVOEHNG-----HVFASYQVSIPOSCQOCL 1650
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 305 KRIKKGKSLKCRDQCVSHPECRDRCPICPTL--IGTP--VKIGE--GMLDQFVQSPTP 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1651 SYIMLMDKRLCSVCMMTCCHKCVHKIQSHCSYTYGRKQEPQAPQHPQCVDSLTSDXA 1710
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 361 MIPSIYVHCNEIEQRGLTETGLYRISGCDRTVKELEKEFLVKTVPVLSKYVD--IHAI 418
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1711 SVPIYLEKLEHVENHGLTTEGLYRKSGAANTRRELQ---ALQTDPAVVKLENFPIHAI 1767
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 419 GLLLDQFLNLKEPLITFPLNRAFMFAEITDEDNSIAAMYQAVGELPQANDRTLAFLMI 478
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1768 TGVCLKOMLELEPEPLMTFAQYGFLEAVELPEKQEQALAIYAVLEHLPANHNSLERLI 1827
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 479 HIGQVA-QSPHTKMDVANAKVGPPTIVAAVNPDPVMSODIKQKQPVVERLLSLPIE 537
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1828 HLVKVALLEDVNMSEFGALAIIFAPCLL-RCPDNSDPLTSMKQVLEKITTCVEMLLEIQQR 1886
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 538 YVSQFMVVEQENIDPLHVIEN-----SNAFSTPQTPD-----IKVSLGPLYT 579
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1887 KKK---VAMEBISQLEAABESIAFRRLSLRQNAANSPTREBAGAGRLTTSRVS-- 1940
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 580 TPEHOLLKTPSSSSLSQVRST-----LTKNTR 608
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1941 SPSTRMLALGSWRSAALRTRGTRPARPGARALRRPR 1980
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7

S29128

N-chimerin - rat

N:Alternate names: GTPase-activating protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S29128; S25152

R:Lim, H.H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.

Biochem. J. 287, 415-422, 1992

A:Title: Developmental regulation and neuronal expression of the mRNA of rat n-chimerin

A:Reference number: S29128; PMID:93074974; PMID:1445199

A:Accession: S29128

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-334 <Lim>

A:Cross-references: UniProt:P30337; EMBL:X67250; NID:G55939; PIDN:CAA47672.1; PID:G55940

R:Lim, H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.

submitted to the EMBL Data Library, July 1992

A:Description: Rat n-chimerin a p21rac GAP:cDNA sequence developmental regulation and n

A:Reference number: S25152

A:Accession: S25152

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-334 <Lim>

A:Cross-references: EMBL:X67250; NID:G55939; PIDN:CAA47672.1; PID:G55940

F:81-130/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match 10.1%; Score 329; DB 2; Length 334;

Best Local Similarity 32.4%; Pred. No. 1,7e-13;

Matches 91; Conservative 46; Mismatches 118; Indels 26; Gaps 8;

```

Qy 259 STLNSRQLEPRTETDSVGTPOSGMGRLHDPVSKTVIKPESCVPGKRIKRGKLS--LKC 316
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 ATLKENEDQIPKYE-----KVHNEFVHTFRGPHWCEYCA-NEMWGLIQGVNC 111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 317 RDCRVVSHPECDRCPLPCITPLTIGTPVKIGEMLADFVSQSPMIPISVHCVNEIEQR 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 ADCGLNVHKQCSKMPNDCKPDLKHVK-KVYSCDLITLVKAITTRPVMVDMCIREISER 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 377 GLTETGLYRISGCDRTVKELEKEFLR--VKTVPVLSKYVDIHAIQSLKDFLRNKEPLL 434
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 GLNSGLYRVSGFSDLIEDVKMAFDRDEKADISVMYEDINIIIGALKLYFRDPIPLI 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 435 TFLRKAPFWEAEITDEDNSIAAMYQAVGELPQANDRTLAFLMIHLQRAQSPHKK--M 491
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 YDVAVPKPIESAKIVDPQOETLHEALRSPLPAFCETLRVMAHLKRV--TLHEKENIM 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 492 DVANLAKVGPPTIVAAVNPDPVMSODIKQKQPVVERLL 532
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 SAEINIGIVGPFLMS--PELDMAALNDIRQRLVVELLI 327
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 8

S08242

N-chimerin - human

N:Alternate names: GTPase-activating protein

C:Species: Homo sapiens (man)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Mar-2004

C:Accession: S08242

R:Hall, C.; Montfries, C.; Smith, P.; Lim, H.H.; Kozma, R.; Ahmed, S.; Vanniasingham, V.; J. Mol. Biol. 211, 11-16, 1990

A:Title: Novel human brain cDNA encoding a 34,000 Mr protein n-chimerin, related to b

A:Reference number: S08242; PMID:90133942; PMID:2299665

A:Accession: S08242

A:Molecule type: mRNA

A:Residues: 1-299 <Hall>

A:Cross-references: EMBL:X51408; NID:G35012; PIDN:CAA35769.1; PID:G35013

F:46-95/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match 9.9%; Score 322; DB 2; Length 299;

Best Local Similarity 32.0%; Pred. No. 4e-13;

Matches 90; Conservative 48; Mismatches 117; Indels 26; Gaps 8;

Qy 259 STLNSRQLEPRTETDSVGTPOSGMGRLHDPVSKTVIKPESCVPGKRIKFKLS--LKC 316
 :
Db 31 ATLKENEDQIPKYE-----KIHNFVHTFRGPHWCEYCA-NEMWGLIQGVNC 76
 :
Qy 317 RDCRVVSHPECDRCPLPCITPLTIGTPVKIGEMLADFVSQSPMIPISVHCVNEIEQR 376
 :
Db 77 ADCGLNVHKQCSKMPNDCKPDLKHVK-KVYSCDLITLVKAITTRPVMVDMCIREISER 135
 :
Qy 377 GLTETGLYRISGCDRTVKELEKEFLR--VKTVPVLSKYVDIHAIQSLKDFLRNKEPLL 434
 :
Db 136 GLNSGLYRVSGFSDLIEDVKMAFDRDEKADISVMYEDINIIIGALKLYFRDPIPLI 195
 :
Qy 435 TFLRKAPFWEAEITDEDNSIAAMYQAVGELPQANDRTLAFLMIHLQRAQSPHKK--M 491
 :
Db 196 YDVAVPKPIESAKIVDPQOETLHEALKLPAFCETLRVMAHLKRV--TLHEKENIM 253
 :
Qy 492 DVANLAKVGPPTIVAAVNPDPVMSODIKQKQPVVERLL 532
 :
Db 254 NAEINIGIVGPFLMS--PELDMAALNDIRQRLVVELLI 292
 :

RESULT 9

A43953

N-chimerin - common canary

N:Alternate names: protein kinase C homolog [misidentification]; song control circuit pr

C:Species: Serinus canaria (common canary)

C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 15-Mar-2004

C:Accession: A43953

R:George, J.M.; Clayton, D.F.

Brain Res. Mol. Brain Res. 12, 323-329, 1992

A:Title: Differential regulation in the avian song control circuit of an mRNA predicting


```

QY 407 PLSKVD-----DI-----HATSLKDFELNKEPLTFLNARAMEAE-----ITDE 451
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 717 KLCTALENGMLVDISEPSSHDCVLYKLRQPEPFLTRKYEITDLAKETQHNNE 776
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 452 DNS-----IAAMYQAVGELPOANRDTLAFMLTLQRYA--QSPHTX 490
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 777 QETKNSLDEKKEPMPCIEINRILKSKDILRQIPASPNFSLHPLVHLKRVVDHAENK 836
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 491 MDVANLAKVEGPTVAHAVPNPD--PYTMSQ--DIKQPKVVELLSLPEYMGQFM--- 543
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 837 MNSKULGVTFEBSLRL--PRPQAPITISLSLAYSNQARLVEFLIT---YQKLEFDG 888
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 544 -MVEQENIDPLHVIENS--NAFSTPQTPEDIKVLLGVTTPHQHLKTBSSSSLSQVRV 599
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 889 SLQPDVWCVCSIGVVDQGFCKPLLSPBERDIERMKSLFESSKXDIHTSESEKSLIFERAT 948
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 600 STLRKNTFRBSKSKSASATNLGR 621
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 949 S-----FEESERKQNALGK 962
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 12
S29956
beta-chimerin - rat
N:Alternate names: GTPase-activating protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A45485, S31398, S29956
R:Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 268, 3813-3816, 1993
A:Title: Gem cell beta-chimaerin, a new GTPase-activating protein for p21rac, is specific
A:Reference number: A45485, MUID:93179371, PMID:8440677
A:Accession: A45485
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-295 <LEU>
A:Cross-references: UNIPROT:003070; EMBL:X69469; NID:957526; PIDN:CAA49244.1; PID:957527
A:Experimental source: testis
A:Note: Sequence extracted from NCBI backbone (NCBIP:125731)
R:Leung, T.; How, B.E.; Manser, E.; Lim, L.
Submitted to the EMBL Data Library, November 1992
A:Description: Gem cell beta-chimaerin, a new GTPase-activating protein for p21rac, is
A:Reference number: S31398
A:Accession: S31398
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-295 <LEU>
A:Cross-references: EMBL:X69462; NID:955816; PID:955817
A:Domain: protein kinase C zinc-binding repeat homology <K2>
;42-91

	Query March	9.1%, Score 294; DB 2;	Length 295;
	Best Local Similarity	29.3%; Pred. No. 2.3e-11;	
	Matches	81; Conservative	52; Mismatches 11; Indels 32; Gaps 8;
Qy	285 RLHDFVSKTVKPPSCVPCGGRIRKEFGKLS--LKCRDRVVSHPECRDRCPLPCTIGT	342	
	: : :	:	
Db	40 KTHNFKYHTFPGPHMCECA-NFMWGLLAGVRSDSGIANHKCCSNHVPRNDQPDLR1	98	
	: : :	:	
Qy	343 PVKIGEGMLADPVQSOTSPMIPSIYVHCYNEIEORGLTETGYRISGCDRTVKELKEFLR	402	
	: : :	:	
Db	99 K-KYYCCDLTLVKAHMTQRPMVVDICIREIARGLSEGGYRVSGTEHIEDVKMFDR	157	
	: : :	:	
Qy	403 VKTVPLSLKYD-----DIHAICSLKDPIRNKKEPLTRNLRAEMEAERIDEDENSI	455	
	: : :	:	
Db	158 DG----EKADISANIYPDINITGALKLYPRDRIPIPTIVDYTKLEIAAKISNAERL	212	
	: : :	:	
Qy	456 AAMTQAVGEPLPOANDRLTAFLMIHLQRYAOSPHTK-MDVANLAKVFPTIIAAHAVPNPD	514	
	: : :	:	
Db	213 EAYHEVMLTLPRAHYETIRYLIMHLKKVTNMKNKNMAEALGIIVFQTLM--RPEDST	270	
	: : :	:	
Qy	515 VTMQDILQPKQVERLLSLPLEYWSQPMVEQENI	550	
	: : :	:	

Db 271 LTTLDHMRKQKLIQV-----ILINEDV 293

RESULT 13

B53764

beta2-chimerin, cerebellar - rat (fragment)

N/Alternate names: GTPase-activating protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 04-Apr-2004

C/Accession: B53764

R/Leung, T.; How, B.E.; Manser, E.; Lim, L.

J/BIOL. Chem. 269, 12868-12892, 1994

A/Title: Cerebellar beta2-chimerin, a GTPase-activating protein for p21 Ras-related Rac

A/Reference number: A53764; MUID:94230370; PMID:815705

A/Accession: B53764

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-443 <LEU>

F/34-114/Domain: SH2 homology <SH2>

F/190-239/Domain: protein kinase C zinc-binding repeat homology <K2>

[illegible]

```

RESULT 14
A:53764
beta2-chimerin, cerebellar - human
N:Alternate names: GTPase-activating protein
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53764
R:Jeung, T.; How, B.B.; Manser, E.; Lim, L.
J. Biol. Chem. 269, 12888-12892, 1994
A>Title: Cerebellar beta2-chimerin, a GTPase-activating protein for p21 Ras-related Rac
A:Reference number: A53764; MUID:94230370; PMID:8175705
A:Accession: A53764
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-466 <LEU>
A:CIO88-References: UNIPROT:P52757; GB:L29126; NID:g457229; PIDN:AAA191.1; PID:g457230
F:157-137/Domain: SH2 homology <SH2>
F:213-262/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match          9.1%; Score 293.5; DB 2; Length 466;
Best Local Similarity 25.7%; Pred. No. 4.7e-11;
Matches 98; Conservative 66; Mismatches 155; Indels 63; Gaps 12;

Oy 199 KKTIRSGSANDQGNESIVAKTIVTVPNDDGPIEIVASTIEIVP-----YWTRRRRKRGTL 252
db 116 KRFSIHDLVTDGLITLYETKAA-----EYISKMTNPIYEHIGVATLLREIV--- 164

```

QY 253 QPNSSTLNSRLEPR-----TETDSVGTPOSNGM-----RLHDFVSKT 293
 DB 165 -----SRRLSRSGNREPKTNTVTHEHTAVKISSLYRRALITNDNHNFEYKTHKVTHT 219
 QY 294 VIKESCVPCGKRIKKGKLS--LKCRDRCRVSHPECDRCPLPCIPPLITPVKIGGM 351
 DB 220 FRGPHHCEYCA-NFMWGLAQVRCSDGCMVHKQSKHVPNDQCPDLKRIK-KVCCDL 277
 QY 352 ADFVSQSPMIPSIIVHCVNIEIQRGLTETGLYRISGCDRTVKEKEFLR-VKTVPL 409
 DB 278 TLLVKAHNRQRPVNVVICIREIARGLKSGLYRVSGFTSHIDVYMAFRDEKADISA 337
 QY 410 SKYDDIHAICSLKDLPLRNKEPPLTFLNRAFMEEAETDEDNLSAAMYQAVGELPQAN 469
 DB 338 NVYPDINIITGALKLYFRDLPIPVITYDYTSKEFIDAKISNADERLEAVEHVLMLPPAH 397
 QY 470 RDLTALMTLQHVASPHTK-MDVANLAKVPGPTVAHAPNPDPVYMSQDIKROKPY 528
 DB 398 YETLRALMTLHKVTNMEKDNFMNAENLGVFGPTLM-RPPEDSTLTLLHDMRYOKLIV 455
 QY 529 ERLISLPLEYMSQPMVQENI 550
 DB 456 Q-----ILLIENEDV 464

RESULT 15
 D59435
 Gem-interacting protein (imported) - human
 C.Species: Homo sapiens (man)
 C.Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
 C.Accession: D59435
 R.Arresta, S.; Beranger, F.; Berger, R.; de Gunzburg, J.
 submitted to Genbank, November 2000
 A.Description: GMIP, a Gem interacting protein.
 A.Reference number: D59435
 A.Accession: D59435
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-970 <ARB>
 A.Cross-references: UNIPROT:Q9P107; GB:NP_057657; PID:g7706107; PIDN:NP_057657.1

Query Match 9.0%; Score 291, DB 2; Length 970;
 Best Local Similarity 22.6%; Pred. No. 1.9e-10;
 Matches 188; Conservative 112; Mismatches 273; Indels 260; Gaps 40;
 QY 13 EOLVRREVLSEGENVQFIQAKDFEDERK--W--QRDHELKGYKDLIMKAEPTERSA 67
 DB 81 EELDLRL-IRTKGVDAALRYAKTWSRYAKELLAMTEKRASYELDEPAKSTMTKTAENGKVS 139
 QY 68 LDVK-----LKH-----ARQVDVE----- 82
 DB 140 IQQSHMPLQIYITLFLHDLISGLTAMETVAQQKDYQPLAKRTIEIKMKRKEPKQW 199
 QY 83 IKRQRAEDACEKLER-QIQLIR--EMLMCDTSGSIQLEEQKSAALFLNRGQPSNNAG 139
 DB 200 MKQOKMNEAVQALRRRAQLQYORSBELLARSQSPEDSAPQAS-----FGPSKQ 250
 QY 140 NKRSLTIDSGSLISIPKTDSESLDWSLVKTFLLKRE---KRKST--RQFV-D 192
 DB 251 ERRRRSRREBQA-----KAQEAELVQACVREANARQODLEIAKQRTVSHVRKLVFQ 302
 QY 193 GPPGPKTKRSI-----GSAVDQGNESI VAKTIVTPNDG-----PIE 231
 DB 303 GDEVLARVLTSLFLGAGQAQERGPRAFAALAECCAPPEPQRYQEFVRLARPEAPPPPP 362
 QY 232 AVSTIETVYWTSS-----RKKTGTLQ-----PNNSDST---LNSRQLEPRTE 271
 DB 363 AFGFOEFLSLNSPLDIRKKLSGPLRPRLDENSABEGPWEDPOTGWRQGTGPTPGSD 422
 QY 272 TDSVG-----TPQNGMRLHDPVSKTVIKPESC-----VPCGKRIKF 309
 DB 423 VDSVGGSGSEBSRLSDPTSSPGAGTROLVKASSTGTSTSSDDPEERDPLGDLNGLGSPF 482

QY 310 GKLSL-----KCRDRC--VSHPECDR---RCPLPCIPPLI----- 340
 DB 483 GKWTLSAQAQTHQLRLRGPACRCECAFMVSGTECECFLLCHKRCLFTLLILCGHRL 542
 QY 341 --GTPKIGGM-----ADFSQSPMIPSIIVHCVNIEIQRGLTETGLYRISGCDRTVKE 395
 DB 543 PARTPL-FGVDFQLPRDPPEE---VPFVYKCTAEIHRALDVQGIYKVSRRVVER 597
 QY 396 LKEKFLRVKTVPLLSKYDDIHAICSLKDLPLRNKEPPLTFLNRAFMEEAETDEBD--- 452
 DB 598 LQCAFENGALVBLSG-NSPHDVSSVLKRFLOELTEPVI-PFHLYDAFISLAKTLHNDPGD 656
 QY 453 -----NSIAAMYQAVGELPQANRDTLAFMLTLQRY-AQSPTKQDVANLAKVFGP 502
 DB 657 DPGTPSPSPDVIRSLKTLIVQLPDSNYNTLRLHLVHLFRVAARFMENKMSANNLGIYFGP 716
 QY 503 TIVAHAVPRPD-----PYMSQDIKXQPKVVEHLISLPLEYMSQPMVQENIDPLH 554
 DB 717 TLLR---PPDGPRASALPVYTCLLDSGHQAOQV-----PLIVHYEQIFGMD 760
 QY 555 VIENSNAFSTPQTPDIKVLGFPVT-----PEHQ---LTKTPS-----SSSLSQ 596
 DB 761 ELRPQ-----ATEPPQDPSPAPRGPLTSSQPRPHLDPSQRPVLAADPGDPQGHSTLBO 816
 QY 597 RVRSTLTK-NTPRFGSKSKATN-----LGRQ--GNFPASP 629
 DB 817 HPTATPTETIPQSDQREDAEDTKDGGEVSSQGPEDSLTGTQSRGHFSRCP 869

Search completed: February 1, 2005, 14:20:01
 Job time : 57 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:09:12 ; Search time 40 Seconds
(Without alignments)
1047.824 Million cell updates/sec

Title: US-09-881-736a-2

Perfect score: 3243

Sequence: 1 MPTMMLNVLNLEPQLVRVE.....SKSATNIGRGQNFPAAPMLK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A-COMB.pep: *
2: /cgn2_6/prodata/1/iaa/5B-COMB.pep: *
3: /cgn2_6/prodata/1/iaa/5A-COMB.pep: *
4: /cgn2_6/prodata/1/iaa/5B-COMB.pep: *
5: /cgn2_6/prodata/1/iaa/PCTUS-COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	9.3	1261	US-09-080-855-2	Sequence 2, Appl1
2	301	9.3	1261	US-09-566-076-2	Sequence 2, Appl1
3	270.5	8.3	2548	US-09-172-422-1	Sequence 1, Appl1
4	257.5	7.9	165	PCT-US93-03076-10	Sequence 10, Appl1
5	230	7.1	140	PCT-US93-03076-9	Sequence 9, Appl1
6	214.5	6.6	547	US-09-855-323-15	Sequence 15, Appl1
7	210	6.5	1513	PCT-US93-03076-2	Sequence 2, Appl1
8	202.5	6.2	946	US-09-538-092-1230	Sequence 1230, App
9	200.5	6.2	1702	US-09-854-133-434	Sequence 434, App
10	198.5	6.1	645	US-10-164-595-40	Sequence 40, Appl
11	197.5	6.0	638	US-10-164-595-73	Sequence 73, Appl
12	195.5	6.0	537	US-09-270-767-32573	Sequence 32573, A
13	195.5	6.0	537	US-09-270-767-47790	Sequence 47790, A
14	192	5.9	333	US-09-507-765-32	Sequence 32, Appl1
15	192	5.9	433	US-09-507-765-30	Sequence 30, Appl1
16	191	5.9	433	US-09-507-765-31	Sequence 31, Appl1
17	191	5.9	2071	US-09-415-522-6	Sequence 6, Appl1
18	188.5	5.8	439	US-09-507-765-33	Sequence 33, Appl1
19	186	5.7	159	US-09-248-796A-14549	Sequence 14549, A
20	183.5	5.7	162	PCT-US93-03076-8	Sequence 8, Appl1
21	179.5	5.5	581	US-09-270-767-33206	Sequence 33206, A
22	179.5	5.5	581	US-09-270-767-48423	Sequence 48423, A
23	172	5.3	362	US-09-270-767-41652	Sequence 41652, A
24	169.5	5.2	1007	US-09-538-092-736	Sequence 736, App
25	161	5.0	1013	US-09-415-522-8	Sequence 8, Appl1
26	151	4.7	282	US-09-248-796A-20596	Sequence 20596, A
27	150.5	4.6	197	US-09-270-767-33381	Sequence 33381, A

28	150.5	4.6	197	4	US-09-270-767-48598	Sequence 48598, A
29	150.5	4.6	216	4	US-09-513-999C-5155	Sequence 5155, Ap
30	146	4.5	274	4	US-09-248-796A-20527	Sequence 20527, A
31	146	4.5	304	4	US-09-248-796A-20526	Sequence 20526, A
32	140.5	4.3	567	4	US-09-270-767-33051	Sequence 33051, A
33	140.5	4.3	567	4	US-09-270-767-48268	Sequence 48268, A
34	139	4.3	422	4	US-09-248-796A-14141	Sequence 14141, A
35	138	4.3	162	4	US-09-270-767-33895	Sequence 33895, A
36	138	4.3	387	4	US-09-248-796A-20549	Sequence 20549, A
37	133	4.1	724	4	US-09-248-796A-20549	Sequence 179, App
38	131.5	4.1	119	4	US-09-621-976-7641	Sequence 7641, Ap
39	130.5	4.0	667	4	US-10-138-701-24	Sequence 24, Appl
40	129	4.0	1505	4	US-09-538-092-1102	Sequence 1102, Ap
41	128.5	4.0	878	3	US-09-735-934A-2	Sequence 2, Appl1
42	128.5	4.0	878	4	US-10-060-332-2	Sequence 2, Appl1
43	128.5	4.0	878	4	US-10-339-657-2	Sequence 2, Appl1
44	127.5	3.9	204	4	US-09-270-767-56893	Sequence 56893, A
45	127.5	3.9	1354	3	US-08-685-871-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-09-080-855-2
; Sequence 2, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saraa, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heidlo, Carl-Henrik
; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-2

Query Match          9.3%; Score 301; DB 3; Length 1261;
Best Local Similarity 22.4%; Pred. No. 7.9e-19;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;

QY      9 RNLEPQLVRVEVLISGNEVOFIQLAKDPEDFRKKQKRDHE LGKYKULMAETERSA 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      372 RLREBALQKVE---EADELYKV-CVTNVEERRNDVENTKRETLAQLTLVFOCDLTLXA 427

QY      68 LDVFLKHARNOVDVEIKRORBAEADCEKLERQQLIRELMCMCTSGSISLSEBOK---SA 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      428 VTNLNLHMGHLQAASLADRLQSLCGSAKLYDEQGESEFVKATNS-----TEBEKVDGV 482

QY      125 LAFNLNGOPSSSNAGNKRLLSTI---DESGIISLDSIFDKTDESLWDSSLVKTKLKE 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      483 NKLHNSQPSGFGFPANSLSDVVRLPDSSNKKIEEDRCSNADIT---GPGFIRWTFGWMS 539

QY      182 KRRTSRQVVDGPPGVKTRISGSAVDDGNSIYAKTTVYPNDGPIEAVSTIETVY 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      540 DSEST-----GSSSSRSISLDS-----BSI-----SGGD----- 562

QY      242 WTRSRKKTGLPWNDSLTNSKOLEPRTET---DSVGTPOS---NGAMRLHDFVSKTVIX 296
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      563 FHKLPRTSSGMSADDLDEHEPSPSEIGNSLGTIRKKTLMSCAALTHKF--RKLS 620

QY      297 PESCVBCGRKIKFKGLSLKCRDCRVVSHPECRDCLPC---IP---TLIGTVKIGBO 349
```

```
Db 621 PTKCRDCEGIVF--QGVECECLVCHKCKLENLVIICGHOKLPCKIHLFG----- 670
Qy 350 MLADF--VSQSP-MIPSIYVHCNEIEORGLTETGLYRISGCDRTVXELKEKFLRVKT 406
Db 671 --AEFTLVAKKRPDGIPIFLKICASEIENRALCLGIVYVCG-----NKIKTE 716
Qy 407 PLISKVD-----DI-----HAICSLKDFLNLKEPILITFLRNAPMEAE--ITDE 451
Db 717 KICLALENGMHLVDISEFSSHDICDLKLYRQLPEPFIPLYKEFIDLAKELQHVNE 776
Qy 452 DNS-----IAMYQAVGELPOANDTLAFIMIHQRYA--QSPHTK 490
Db 777 QETKNSLEDKKWPMKCIENRILKSKDLRQLPASNPNLSHFLIVHLKRVVDHAEENK 836
Qy 491 MDVANLAKVFPTIVAHAVPNPD--PTMSQ--DIKQPKVERLLSLPLEYWSQFM-- 543
Db 837 MNSKVLGVIFGFSILR---PRQTAPIITISLSAEYNGARLVEFLIT-----YSQKIFDG 888
Qy 544 -MVEQENIDPLAVIENS--NAFTPQTPDIKVSILGPTTPEHQLLKTPSSSSLSQVR 599
Db 889 SIQPDVWMSIGVVOGCEPKPLSPBERDIERSMKSLFFSSKEDIHTSESESKIFERAT 948
Qy 600 STLTKNTPRFGSKSATNLGR 621
Db 949 S-----FESEKQNALGK 962
```

RESULT 2
US-09-566-076-2
Sequence 2, Application US/09566076

```
Patent No. 6475775
GENERAL INFORMATION:
APPLICANT: Sartas, Jan
APPLICANT: Franz, Petra
APPLICANT: Aspenstr, Pontus
APPLICANT: Helman, Ulf
APPLICANT: Genez, Leonel Jorge
APPLICANT: Heidlin, Carl-Henrik
TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL
FILE REFERENCE: 10461/7030
CURRENT APPLICATION NUMBER: US/09/566,076
CURRENT FILING DATE:
EARLIER APPLICATION NUMBER: 09/080,855
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1261
TYPE: PRT
ORGANISM: Homo sapiens
US-09-566-076-2
```

Query Match 9 3%; Score 301; DB 4; Length 1261;

Best Local Similarity 22.4%; Pred. No. 7.9e-19; Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;

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Qy 9 RNLFQOLYRVRVILSEGNVQFIOLAKDFEDFRKKQRTDHE-IGYKDLIMKAETERSA 67
Db 372 RLLEBALQKVE---EADLLYK-CYTNVEERRNDVENTKRELIAQRLTLVQCDLITLKA 427
Qy 68 LDVYKLKHAHQVDEIKRQRAADCEKLERQIQLIREMLKCDTSGISQLSEBQK--SA 124
Db 428 VYVNIFFMHQHLQAAISLADRLQSLCSGAKLYDPQGEVSERFKATNS-----TEBEKVGNV 482
Qy 125 LAFILRGQSSSNAGKRLSTI---DESGISLSDISFDKTDLSLMDSDSLVYTKFLAKKE 181
Db 483 NKLHNSQSGFGGPNASLSDVLRPLPSSNKIEEDRCSNSADIT---GPSFIRSWTFGMS 539
Qy 182 KRSTSRQFVDPGPVGGFKTRSIGSAVDGNEISIVAKTVVPPNDGPIEAVSTIETVY 241
Db 540 DSEST-----GSSSESRSLDS-----ESI-----SPGD----- 562
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Qy 242 WTRSRKKTGTLQPMNSDSTLNSRQLEPRTER--DSVGTPOS--NGKRLHDFVSKTVIK 296
Db 563 FHRKLPRTSPSGTMSADLDERBPSSETEGPNISLGTFTKTLMSKALTHRF--RKLS 620
Qy 297 PESVPCGRIRIKFGSLISKRCRVVSHPECDRCPLPC---IP---TLIGTPVKGIGB 349
Db 621 PTKCRDCEGIVF--QGVECECLVCHKCKLENLVIICGHOKLPCKIHLFG----- 670
Qy 350 MLADF--VSQSP-MIPSIYVHCNEIEORGLTETGLYRISGCDRTVXELKEKFLRVKT 406
Db 671 --AEFTLVAKKRPDGIPIFLKICASEIENRALCLGIVYVCG-----NKIKTE 716
Qy 407 PLISKVD-----DI-----HAICSLKDFLNLKEPILITFLRNAPMEAE--ITDE 451
Db 717 KICLALENGMHLVDISEFSSHDICDLKLYRQLPEPFIPLYKEFIDLAKELQHVNE 776
Qy 452 DNS-----IAMYQAVGELPOANDTLAFIMIHQRYA--QSPHTK 490
Db 777 QETKNSLEDKKWPMKCIENRILKSKDLRQLPASNPNLSHFLIVHLKRVVDHAEENK 836
Qy 491 MDVANLAKVFPTIVAHAVPNPD--PTMSQ--DIKQPKVERLLSLPLEYWSQFM-- 543
Db 837 MNSKVLGVIFGFSILR---PRQTAPIITISLSAEYNGARLVEFLIT-----YSQKIFDG 888
Qy 544 -MVEQENIDPLAVIENS--NAFTPQTPDIKVSILGPTTPEHQLLKTPSSSSLSQVR 599
Db 889 SIQPDVWMSIGVVOGCEPKPLSPBERDIERSMKSLFFSSKEDIHTSESESKIFERAT 948
Qy 600 STLTKNTPRFGSKSATNLGR 621
Db 949 S-----FESEKQNALGK 962
```

RESULT 3
US-09-172-422-1
Sequence 1, Application US/09172422A

```
Patent No. 630485
GENERAL INFORMATION:
APPLICANT: Adams, Arwen E.
APPLICANT: Chiu, Choi Ying
APPLICANT: Duh, David
APPLICANT: Gorman, Susan W.
APPLICANT: Leng, Song
APPLICANT: Sheffield, Val
TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
FILE REFERENCE: 200130.442
CURRENT APPLICATION NUMBER: US/09/172,422A
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2548
TYPE: PRT
ORGANISM: Homo sapien
US-09-172-422-1
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Query Match 8 3%; Score 270.5; DB 3; Length 2548;

Best Local Similarity 24.4%; Pred. No. 2e-15; Matches 130; Conservative 75; Mismatches 203; Indels 125; Gaps 24;

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Qy 143 ISTIESGSIISIDIFDKTDESILMDSDSLVYTKFLKKEKRSTSRQFVDPGPVKKTR 202
Db 1864 LKSMDE--FLKKVN-DLDNDSKCDITVDVYFKALKAEFRQN-----IFERY 1908
Qy 203 SIGSAVDQGN-----ESIVAKTVVVPNDG--GPIEA-VSTIETVPYVTRSGR 247
Db 1909 SSALAMDQKSIKYKDYALFQOILEKTRLEQRDSLGESPVRVWVNTFKVYLDREYMEF 1968
Qy 248 KTGTLQPMNSDSTL-----NSRQLEPRTERTSVGTPOGNGKRLHDFVSKTVIKESQVP 302
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Db 1669 KT-----SDCTATVPTTERKRRKKTDLV--EEHNG---HIFKATQVSIPTCYC 2015
 QY 303 CGKRIKFGKLSKRCDCRVVSHPECHRCGLPCIPITLIGTPVIGE-----GMLADPV 355
 Db 2016 CGLWIMMBASVCKYCKYACHKKC-----CLKTTAKCSKKYDELSSRQGVLSRL 2068
 QY 356 SGTSPMIPSIYVHCVNEIFQRTGTEGLYRISGCDRTVKEKELRVTKTPILSKYD- 414
 Db 2069 TSEDRTVPLVEKLIVIEHGLYEGYRKSSTNIXIKELRQ---GLDDABESVNLDDY 2125
 QY 415 -THATSLKDPRLNKEPLTFRLNRAFMEEAITDEDNSIAAMYQAVGELPOANDTL 473
 Db 2126 NTHVIAVSFKQWRDLPNPLMTLETLYEELRANGLOERKETIGVSVLDQSLRTHLNL 2185
 QY 474 AFIMIHQVVA--QSPHTKMDVANLAKVFGPTIVAHAVPNPDPTWMSQDIREKQPVVERLL 532
 Db 2186 ERLIFLTVRIALQEDNTRMSANALAVFAPCIL-RCPDITDPLQSOVDISKTTCE--- 2241
 QY 533 SLPLEYWSQPMWYQEN-----IDPLHVIENSNAFSTPQTPDIKVSLL----- 575
 Db 2242 -----LIVEQNNKYARLKDLSLEFAENK-----AKTRLDIRSMGKRI 2284
 QY 576 -----GPVTPRHQLKTPSSSLSQRVASTITTKTPRGSKSKATNLGRQ 622
 Db 2285 RRGNYBGP-SSP--VVVRLPSVSDVSB--ETLT-----SEAMETDITEQ 2324
 RESULT 4
 PCT-US93-03076-10
 ; Sequence 10, Application PC/TUS9303076
 ; GENERAL INFORMATION:
 ; APPLICANT: Whitehead Institute for Biomedical Research
 ; TITLE OF INVENTION: GAP-Associated Protein p190 and
 ; TITLE OF INVENTION: Transduction
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: 2 Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Releasee #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/03076
 ; FILING DATE: 19930331
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: WHI92-03A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 165 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US93-03076-10
 Query Match 7.9%; Score 257.5; DB 5; Length 165;
 Best Local Similarity 37.9%; Pred. No. 3,4e-16;
 Matches 64; Conservative 33; Mismatches 63; Indels 9; Gaps 4;
 QY 369 CVAIEIQRGLTETGLYRISGCDRTVKEKELR--VKTVPPLSKVDDIHAIKSLKDFL 426
 Db 1 CIREIEBGRGLNSGLYVSGFSDLIEDVKNAFDRDGEKADISVVMYEDINITGALKLYF 60

QY 427 RNKEPILTRLNRAFMEEAITDEDNSIAAMYQAVGELPOANDTLAFLMIHLQVAAOS 486
 Db 61 RDLPIPLITYDAYPKPIESAKIMDPDEQLETHBAKLLPAPACETLRIMATLKV--T 118
 QY 487 PHTK---MDVANLAKVFGPTIVAHAVPNPDPTWMSQDIREKQPVVERLL 532
 Db 119 LHEKENLMAENLIGVFGPTLMRS--PELDMAAALNDIRYQRLVVELLI 165
 RESULT 5
 PCT-US93-03076-9
 ; Sequence 9, Application PC/TUS9303076
 ; GENERAL INFORMATION:
 ; APPLICANT: Whitehead Institute for Biomedical Research
 ; TITLE OF INVENTION: GAP-Associated Protein p190 and
 ; TITLE OF INVENTION: Transduction
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: 2 Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Releasee #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/03076
 ; FILING DATE: 19930331
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: WHI92-03A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 140 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US93-03076-9
 Query Match 7.1%; Score 230; DB 5; Length 140;
 Best Local Similarity 38.8%; Pred. No. 1.1e-13;
 Matches 54; Conservative 24; Mismatches 59; Indels 2; Gaps 2;
 QY 369 CVAIEIQRGLTETGLYRISGCDRTVKEKELR-LRYKTVPLSKVDDIHAIKSLKDFL 427
 Db 1 CVEIEIRRGMEVGIYRVSQVATDIOALKAFVNNKDVSVMSSEMDVNLACTLKYFR 60
 QY 428 NKEPILTRLNRAFMEEAITDEDNSIAAMYQAVGELPOANDTLAFLMIHLQVAAOS 487
 Db 61 ELPEPLTDEFFYNFEGIALSDPAKESCMNLNLLSPRANLLTFLDLHLKRVAKKE 120
 QY 488 H-TKMDVANLAKVFGPTIV 505
 Db 121 AVNKMGLHNLATVFGPTLL 139
 RESULT 6
 US-09-855-323-15
 ; Sequence 15, Application US/09855323
 ; Patent No. 6602667
 ; GENERAL INFORMATION:
 ; APPLICANT: Walker, Michael G.
 ; APPLICANT: Volkmutz, Wayne

```

/ APPLICANT: Klingler, Tod M.
/ TITLE OF INVENTION: Inflammation-Associated Polynucleotides
/ FILE REFERENCE: PB-0006-1 CIP
/ CURRENT APPLICATION NUMBER: US/09/855,323
/ CURRENT FILING DATE: 2001-05-14
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PERL Program
/ SEQ ID NO 15
/ LENGTH: 547
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: 2471716CD1
US-09-855-323-15

Query Match          6.6%; Score 214.5; DB 4; Length 547;
Best Local Similarity 29.2%; Pred. No. 36-11;
Matches 57; Conservative 34; Mismatches 75; Indels 29; Gaps 3

QY      349 GMLADPV-----SQTSPMIPSIIVHCVNEIEQGLTETGLYRISGCDRTVKELKEK 399
Db      330 GLRDQVGGCQLSICQREGDTPSFLRLCIAAVDKRGDVGIVYSGNLAVVQKLRFL 389
QY      400 FLKXTVPL-----LSKVDIHAISLKLDPFRNKEPLTTRLR 440
Db      390 VDREAAVTSRGYVPEPQGGEGRLDSTEMDDIHVVGALKLFLRELPPQPLVPLLR 449
QY      441 AFMEALETDEDSIAAMVQAVGELPQANRDTLAFIMILQGV-AOSPHTKMDVANLAKY 499
Db      450 HFRALALASESGQCSQIQELGSMKPRHDTLRYLREHLGVIAHSDKNRMTPHNLGIV 509
QY      500 FGPITVAHAVPNPD 514
Db      510 FGPTLFRPEQETSDP 524

RESULT 7
PCT-US93-03076-2
/ Sequence 2, Application PC/TUS9303076
/ GENERAL INFORMATION:
/ APPLICANT: Whitehead Institute for Biomedical Research
/ TITLE OF INVENTION: GAP-Associated Protein p190 and
/ TITLE OF INVENTION: Transduction
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
/ STREET: 2 Militia Drive
/ CITY: Lexington
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/03076
/ FILING DATE: 19930331
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granahan, Patricia
/ REGISTRATION NUMBER: 32,227
/ REFERENCE/DOCKET NUMBER: WHI92-03A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1513 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein

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Query Match	6.5%;	Score 210;	DB 5;	Length 1513;
Best Local Similarity	19.1%;	Pred. No. 4.5e-10;		
Matches 125;	Conservative 99;	Mismatches 224;	Indels 208;	Gaps 27;
QY	67	ALDYKLGKAAHQVDAVEIKRRQRAEAD-----	CEKLEROIQIREML-----	107
DB	892	AIDV-----LDNDLSRQLTEGEEIAQIEDGFTSLICSHQHKLLEFHFPEKQDVE		943
QY	108	-----MCDTSGSIQLUSEBQKSLAFLINRQPPSSNAGNRRLSTIDSGS		151
DB	944	KNIIIEATMYDVAEACSTTEEEVFNSPRAGSPICNSNL-QDSEEDVEPPSYHIFREDAT		1002
QY	152	ILASDISPKTDDESIDMD-----SGLVTFPKLKKREKRRSTRSQFVDGPPGPYKK-----		200
DB	1003	LPRLSDHSHKFSMELEGNDGLSFTIMSNFSSKLNNK-----VPPPVKPKPVHF		1050
QY	201	--TRISGSAVDQGNESIVAKTYTT--VENDG-----GPIEAV-----STIEVVPY		241
DB	1051	EITPDL--SYLDQREGQRKSMSSPMPPDGDPPSDYAPMAVVKPRNEEENIVSVPH		1109
QY	242	WTRERRRKTGLLOPMN-----SDSTLNSQLERPTETDSVGTPOQSGKRLHDFVS		291
DB	1110	-DSIQGKIITIRKINKAQSGNSGNGSDSEMDTSLSEKGRVSA-----VS		1153
QY	292	KTVIKPESCPVPCGK---RIKF-----GKLSLKRCD-----		318
DB	1154	KPVLYTRCTRLGRFASGYSFVSVDDELGIPIRKEEDQASQCYKGDNAVIPIETDEDP		1213
QY	319	-----GRVSHPECRDRCPKPC-----PTLIGTPVKIKGEGMLAFVQSGTSPMR		363
DB	1214	RRRNILSLRRNTKKPKPK---PPPSITKATWESNFGVP-----LTTVVTPERK-IP		1262
QY	364	SIIVHCNNEIEQRIETGTGLYRISGCDRTYKEIKERFLAKTYPLSLKVDIDHAIISLKL		423
DB	1263	IFIERCIIEYIEANGLSREGIYRSGNKSSEMSIQRQDDQDHNIDIAEKDPTVMTVAGAMK		1322
QY	424	DFLNRLKEPLITFLRLNFAFMEAAETDEDSIAAMQAVGELRQANFDTLAFLMIHLQRY		483
DB	1323	SFFSELDPPDPVPSMQIDLVEAHKINDREKHLAKKVLKKFPKEMNEVEKRYVISHLNRV		1382
QY	484	AQSHHTK--MUVANLAKVFGPTIVAAHAVNPDPVTMSODIKRQPKVVERLLS-----		533
DB	1383	SHNNKVALMISENLSICFWPTLAKRPDSSMDALTATRSYQ---TIILFLIQOCPEFFTYNR		1439
QY	534	-----LPLEWYSGFMVWQENIDPLHVIENSNAFSTPQTPDRIKYSVLGPTV		579
DB	1440	PISEPPGALALPQPMHPL-----SPSSPHLL-----PVSHHLPSSHLOPLS		1482
RESULT 8	US-09-538-092-1230			
	Sequence 1230, Application US/09538092			
	Patent No. 6753314			
	GENERAL INFORMATION:			
	APPLICANT: Glot, Loic			
	APPLICANT: Mansfield, Traci A.			
	TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same			
	FILE REFERENCE: 15966-542			
	CURRENT APPLICATION NUMBER: US/09/538,092			
	CURRENT FILING DATE: 2000-03-29			
	PRIOR APPLICATION NUMBER: 60/127,352			
	PRIOR FILING DATE: 1999-04-01			
	PRIOR APPLICATION NUMBER: 60/178,965			
	PRIOR FILING DATE: 2000-02-01			
	NUMBER OF SEQ ID NOS: 1387			
	SOFTWARE: CurataseqFormatter Version 0.9			
	SEQ ID NO 1230			
	LENGTH: 946			
	TYPE: PRT			
	ORGANISM: Homo sapiens			
	FEATURE:			

NAME/KEY: misc_feature
 LOCATION: (0)...(0)
 OTHER INFORMATION: Polypeptide Accession Number P98171
 US-09-538-092-1230

Query Match 6.2%; Score 202.5; DB 4; Length 946;
 Best Local Similarity 21.4%; Pred. No. 1e-09;
 Matches 143; Conservative 99; Mismatches 256; Indels 170; Gaps 27;

45 QRTDH---ELG---KYKDLMKAEKTERSLDVKTKARNOVVEIKRRQRADECKLE 97
 130 QRLSHAEVDGLVKSRLDEQOLDELEVSELQTAKTQAYHNEGVNAEKUREAL 189
 98 RQIQ-LIRELMCDTSGSIQLESEOKSAL-----APLNRCQPSSSNANKRLST 145
 190 ROEKERAGSVPTTGATAGPLRKSSLKGGRLVEKRAKEMHKLCTKXARNEVLS 249
 146 IDBSGSLDISDKTDESIDMDSLVKTFKLRKREKRSRQFVDPGPGVKTRSIG 205
 250 L--ASVNAVASNYVYLDVLDLMDCCDTGPHLAGVLRSTYAAESRTQASQVGLGLE 306
 206 SAVD---QGNESIVAKTIVT-----PNDGPIEAV----- 233
 307 EAVEALDPEDKAKVLEHATVFCPLRPDYHPHDGDEVAEICERELRDEILPRAQNIQ 366
 234 ----STIETVPWTSRRKKTGLQPW-----NSDSTLNSRQLEPRTETDSVGTPOSG 282
 367 SRLDRGTITEEV--NKTILKATLQALLLEVASDDGVDLSFQTSPETE--SLKTSISDP 421
 283 GNR-----LHDFVSKTVIKPESCVPCGKRIKRGKLSLK----- 315
 422 GSRQAGRRCGOQOQETETFYLTQLQEYLS-----GRS1-LAKLOAKHEKLEQAL 468
 316 ---CRDQVVSHEC-----RDRCPICL---PTLIGTPVKIGEGMLADPVQSPTMIP 363
 469 QRGDKKEQESWTQYQRFQKSRQPPSSQVQNRIFG-----GMEKFIQSSGQVPV 521
 364 SIYVHCVNEIEQGLTETGLYRISGCDRTVKELEKEFLRVKTVPLLS--KYDDIHAICSL 421
 522 LVESGIRFINLNGLQHEGIFRVSQAGLRSEIRDAFERED-PLYVGCRAHLDSDVAGV 580
 422 LKDFLNLKEPLLTRLNRAFMBAETIDEDNSIAAMYQAVGELPQANRDTLAFIMHIQ 481
 581 LKLYFRSLRPPPLPPLPFGELLASSELDETAERVHVSRLMLRPAVLVLYLFTFLN 640
 482 RVAG-SPHTKMDVANLAKVGFITVAHAVNPDPVMSQIQKPKVVEVLSLPLEYMS 540
 641 HLAQYSDENMMDPYLAVCGFPTL-----FVPAGQDPVALQGRVQLV----- 684
 541 QFMVMEQENIDPLHVIENSNAFSTPOTPDIKVSLGLGVTTPEHQLKTPSSSSLSQ-RVR 599
 685 QTLIVQPDRIYF-----PLT-----SLPGV--YKCAAPFASCLGDAQLE 724
 600 STLTKNTP 607
 725 SLGADNDP 732

RESULT 9
 US-09-854-133-434
 Sequence 434, Application US/09854133
 Patent No. 6759508
 GENERAL INFORMATION:
 APPLICANT: Lodes, Michael J.
 APPLICANT: Mohamath, Raedon
 APPLICANT: Henderson, Robert A.
 APPLICANT: Benson, Darin R.
 APPLICANT: Secrist, Heather
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121.475C10
 CURRENT APPLICATION NUMBER: US/09/854.133
 CURRENT FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 735
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 434
 LENGTH: 1702
 TYPE: PR1
 ORGANISM: Homo sapiens
 US-09-854-133-434

Query Match 6.2%; Score 200.5; DB 4; Length 1702;
 Best Local Similarity 28.3%; Pred. No. 4.3e-09;
 Matches 72; Conservative 54; Mismatches 95; Indels 33; Gaps 12;

364 SIYVHCVNEIEQGLTETGLYRISGCDRTVKELEKEFLRVKTVPLLSK---VDIHAICS 420
 2 AVLGSCAFIERGIYD-GYRLSGVASNIQRLRHF-DSRHVPDLTKERYVDHSVGS 59
 421 LKDFLNLKEPLLTRLNRAFMBAETIDEDNSIAAMYQAVGELPQANRDTLAFIMHI 480
 60 LCKLYRRELNPPLITQLYKEKFSDAVSAATDEERLKHIDVIOQLPPEPHRYLFLMRHL 119
 481 QRYAG-SPHTKMDVANLAKVGFPTI-----VAHAVNPDPVTSODIKQPKVERLLS- 533
 120 SLADYCSITNMHAKALVAMBNLRSKOIBACFSGRARF--EVRIOSVVEEPLNH 177
 534 LPLEYMSQFMVMEQENIDPLHVIENSNAFSTPOTPDIKVSLGLPVTTPEHQLKTPSSSS 593
 178 VDLVFSGRISMAMQ-----EGAASLSRPK-----SLT--VASPTKLTLLBEAQ 220
 594 LSO-RVRSITL-TQN 605
 221 RTQAVNSPVTEN 234

RESULT 10
 US-10-164-595-40
 Sequence 40, Application US/10164595
 Patent No. 6657054
 GENERAL INFORMATION:
 APPLICANT: Origene Technologies, Inc
 TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
 FILE REFERENCE: 10 103 R1
 CURRENT FILING DATE: 2002-06-10
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 40
 LENGTH: 645
 TYPE: PR1
 ORGANISM: Homo sapiens
 US-10-164-595-40

Query Match 6.1%; Score 198.5; DB 4; Length 645;
 Best Local Similarity 20.2%; Pred. No. 1.3e-09;
 Matches 96; Conservative 77; Mismatches 174; Indels 129; Gaps 18;

166 DMDSLVKTFKLRKREKRSRSTQFVDPGPGVKTRSIGSAVDQGNESIVAKTIVTPN 225
 8 NMD-----FNLKVEAKIARSRVMTG-----EGMAAHFSPSTPN 42
 226 DGGPIEAVSTIETVPWTSRRKKTGLQPNWSDSTLNSQLEPRTETDSVGTPOSGMR 285
 43 ---PLERPIKMG---WLKKQR--SIVKW---QQRVFLVRAQ-----Q 74
 286 LHDVFSKTVIKPESCVPC-GKRIKPKGLSLKCDKCVVSHPERDRCPLPIPT----- 338
 75 LYYKDEBDTPKPGCMYLPDCTIK-----BIATNPEAGFVEEIIIPASWDQR 123
 339 -----LIGTPVKIGEGMLADPVQSOTSP-----MPSIVVHC 369
 124 MGDSYVLAASSQAEMEWKFLRVAAGTFCGFGRLBETAVAYEQKFGHVLPIVVK 183
 370 VNEIEQGLTETGLYRISGCDRTVKELEKEFLRVKTVPLLSKVDIHAICSLKDLPLNL 429

Db 184 AEFIEHGENEIGIFRLPGQDNLVQKLRDAF-DAGERPSPDRDVTHTVASLLKYLRLD 242
Qy 430 KEPLTFRLNRAFMEAETIDEDNSIA--AMTQAVGELPOANDTLAFIMHLOV-AQS 486
Db 243 PEPVPMQSYEGFLCGQLTNDEAKAQOELMKQLSLPRDYSLSLSTICRFLHEIQLNC 302
Qy 487 PHTKDVANLAKVFGPTTVAHVNPDPVTMSQDIKQKQVVERLLSLPLEYWSQFMVE 546
Db 303 AVNKKSVDLATVIGVNLIRSKVEDP-----AVIMRGTPQIQRVMT-----MMIR 347
Qy 547 QENI-----DPLVIENSNAFSTPQTDIKVSLGPTTPEHQLKTPSSSSLS 595
Db 348 DHEVLFPKSKDILSPPAQKN---DPKAPVARSVGMATEDLRISRTDSSFSMT 400

RESULT 11
US-10-164-595-73
; Sequence 73, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: IU 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-595-73

Query Match 6.1%; Score 197.5; DB 4; Length 638;
Best Local Similarity 24.5%; Pred. No. 1.6e-09;
Matches 66; Conservative 53; Mismatches 117; Indels 33; Gaps 8;

Qy 341 GTPVKGEGMLADPVQSOTSP---MPSIVHCVNEIEORGLTETGLYRISGCDRTVKEL 396
Db 144 GTPCGVFGQRLDETVAYEKGFGPHLVPLIVEKCAEILHGNNEBIFRLPGQDNLVQKL 203
Qy 397 KEKFLRKVTVPPLSKVDIHAICSLKDLPLNKEPLTFRLNRAFMEAETIDEDNSIA 456
Db 204 RDAF-DAGERPSPDRDVTHTVASLLKYLRLDPEPVPMQSYEGFLCGQLTNDEAKA 262
Qy 457 --AMTQAVGELPOANDTLAFIMHLOV-AQSPHTKDVANLAKVFGPTTVAHVNPDP 513
Db 263 QOELMKQLSLPRDYSLSLSTICRFLHEIQLNCANVKKSVDLATVIGVNLIRSKVEDP- 321
Qy 514 PVTMSQDIKQKQVVERLLSLPLEYWSQFMVEQENI-----DPLVIENSNAFSTPQ 566
Db 322 ----AVIMRGTPQIQRVMT-----MMIRDHVLFPPKSKDILSPPAQKN---DPK 364
Qy 567 TPDIKVSLGPTTPEHQLKTPSSSSLS 595
Db 365 KAPVARSVGMATEDLRISRTDSSFSMT 393

RESULT 12
US-09-270-767-32573
; Sequence 32573, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32573
; LENGTH: 537
; TYPE: PRT

; ORGANISM: Drosophila melanogaster
US-09-270-767-32573

Query Match 6.0%; Score 195.5; DB 4; Length 537;
Best Local Similarity 22.5%; Pred. No. 1.9e-09;
Matches 92; Conservative 66; Mismatches 172; Indels 79; Gaps 17;

Qy 258 DSTLNSRQLEPRTEDSVGTPOSGMRLHDFVSKTVIKPES-----CVPGCKR- 306
Db 128 DSTNTAVLVSNSTSIDVCSNSSGG-----SPAVGSKSGRDRNGLIECCSSCKRW 180
Qy 307 --IKFGKSLKCRDQVVS---HPECRDRCPLPCIPPLIGTPVKI-----GEGMLAD 353
Db 181 HDLKQRMHTLE-QDLLVQTTYQLEHQKSGCC-TLAPGLDBPVQVQSGOTGRGRCGS 238
Qy 354 FVSQTSPP-----MPSIVHCVNEIEORGLTET---GLYRISGCDRTV 393
Db 239 ASSSTKPCPDTELEWVLKHDQRTVPRIYVDDCCDILEQKRRSTQPIBGIYQCGDYNKI 298
Qy 394 KELKEKFLRKVTVPPLSKVD-DIHAICSLKDLPLNKEPLTFRLNRAFMEAAB--IT 449
Db 299 QTLRFS-IDANDYDRLQPDVDIHTLGTGLKFLREIKSPLVRVNEAKTFIGQPNQWLLT 357
Qy 450 DEDNSIAAMYQAVGELPOANDTLAFIMHLOVQAQSPHTKDVANLAKVFGPTTVAHV 509
Db 358 DLSAKLDSIKRLIRSLPESNRDMDYIFGHFMRITKVPLOQISAEPLSISVPSIF-HTV 416
Qy 510 PNPDPVTMSQDIKQKQVVERLLSLPLEYWSQFM--MVEQENIDPLHVI---ENSNAFST 564
Db 417 PQGVHMQDIOQLLRGEFTLADCVKLMTEYQGIIFRLNPHRPSPTWAVANGSNPLRN 476
Qy 565 PQTPIK--VSLGPTT-----PEHQLKTPSSSSLSQVR 598
Db 477 PEIPISTRKRETPQLVPLATTSYFNSPNSRYKSMFESKIPGSTHRTYRI 525

RESULT 13
US-09-270-767-47790
; Sequence 47790, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47790
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47790

Query Match 6.0%; Score 195.5; DB 4; Length 537;
Best Local Similarity 22.5%; Pred. No. 1.9e-09;
Matches 92; Conservative 66; Mismatches 172; Indels 79; Gaps 17;

Qy 258 DSTLNSRQLEPRTEDSVGTPOSGMRLHDFVSKTVIKPES-----CVPGCKR- 306
Db 128 DSTNTAVLVSNSTSIDVCSNSSGG-----SPAVGSKSGRDRNGLIECCSSCKRW 180
Qy 307 --IKFGKSLKCRDQVVS---HPECRDRCPLPCIPPLIGTPVKI-----GEGMLAD 353
Db 181 HDLKQRMHTLE-QDLLVQTTYQLEHQKSGCC-TLAPGLDBPVQVQSGOTGRGRCGS 238
Qy 354 FVSQTSPP-----MPSIVHCVNEIEORGLTET---GLYRISGCDRTV 393
Db 239 ASSSTKPCPDTELEWVLKHDQRTVPRIYVDDCCDILEQKRRSTQPIBGIYQCGDYNKI 298
Qy 394 KELKEKFLRKVTVPPLSKVD-DIHAICSLKDLPLNKEPLTFRLNRAFMEAAB--IT 449
Db 299 QTLRFS-IDANDYDRLQPDVDIHTLGTGLKFLREIKSPLVRVNEAKTFIGQPNQWLLT 357

```

QY 450 DEDNSIAAMYQAVGELPOANRDTLAFIMHLOEVAOSPHTKMDVANLAKVGPITIAHAV 509
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 358 DLSAKDLSKRLRLRSIPESNRDTMDYIFGHFNRTIKVPLQOISAEPLSISVTSIF-HTV 416
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 510 PNPDPVTMGODIKRQKRVVERLLSLPLEYWSQPM--MVEQENIDPLHVI---ENSAFST 564
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 POGVHMDIQQLRREGETLADCVKLMIEYQGRIFDRLRPHRPSPTWAVVANGSGNPLRN 476
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 565 PGPDPK--VSLGPEVT-----PEHQLKTPSSSSLSQSV 598
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 477 PEIPSTRKEETPOLVPLATTISYPNSPNRKYPSKWSKIPGSIHRTYRI 525
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

```

US-09-507-765-32
; Sequence 32, Application US/09507765
; Patent No. 6509155
; GENERAL INFORMATION:
; APPLICANT: Klingert, Tod M.
; APPLICANT: Stewart, Elizabeth A.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
; FILE REFERENCE: PC-0010 US
; CURRENT APPLICATION NUMBER: US/09/507,765
; CURRENT FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6509155 96572185
US-09-507-765-32

```

Query Match 5.9%; Score 192; DB 4; Length 333;

```

Best Local Similarity 26.6%; Pred. No. 1,8e-09;
Matches 78; Conservative 46; Mismatches 109; Indels 60; Gaps 12;

```

```

QY 325 PEGRDRCPICPIPT-LIGTPVKIGEGMLADPVSQTSPIVHCVNEIBORGLTETGL 383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 PPTKTPPPRPPLPTQOFGVSLQ---YKLD--KNQGELIPVLRFTVTLREKGLRTEGL 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 384 YRISGCDRTVKEKEKFLKVTVPPLSKYDDIHAICSLKDPRLNKEPLTFRLRATM 443
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 FRRSASVQTVREIQRLYNQKPVN-PDDYGDHIIPAVILKTFRLRPLPQLTF---QAYE 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 444 EAAEITDEDNS--IAAMYQAVGELPOANRDTLAFIMHLOEVA--QSPHTKMDVANLAKVF 500
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 QILGITCVSSSLRVTCGQILRLSLPEHNYVTLRYLMGFLHANSRESIFNKMSSNLACVF 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 501 GPTIAHAVNPDPVTMGODIKRQKRVVERLLSLPLEYWSQPMVEQENIDPLHVIENS 560
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 GNLN-----IMPSQGVSSLSLV-----PLNMFTELLIEYEKI----- 280
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 561 ARSTPOTPIKVSLLGPVTTPEHQL-----KTPSSSSLSQSVRSTLTXT 606
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 281 -FSTPEAPG-----EHGLAPWEGSRAAPLOEAVPRTQATGLTKPT 320
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15

```

US-09-507-765-30
; Sequence 30, Application US/09507765
; Patent No. 6509155
; GENERAL INFORMATION:
; APPLICANT: Klingert, Tod M.
; APPLICANT: Stewart, Elizabeth A.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS

```

```

; FILE REFERENCE: PC-0010 US
; CURRENT APPLICATION NUMBER: US/09/507,765
; CURRENT FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6509155 3068538CD1
US-09-507-765-30

```

Query Match 5.9%; Score 192; DB 4; Length 433;

```

Best Local Similarity 26.6%; Pred. No. 2,8e-09;
Matches 78; Conservative 46; Mismatches 109; Indels 60; Gaps 12;

```

```

QY 325 PEGRDRCPICPIPT-LIGTPVKIGEGMLADPVSQTSPIVHCVNEIBORGLTETGL 383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 PPTKTPPPRPPLPTQOFGVSLQ---YKLD--KNQGELIPVLRFTVTLREKGLRTEGL 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 384 YRISGCDRTVKEKEKFLKVTVPPLSKYDDIHAICSLKDPRLNKEPLTFRLRATM 443
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 FRRSASVQTVREIQRLYNQKPVN-PDDYGDHIIPAVILKTFRLRPLPQLTF---QAYE 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 444 EAAEITDEDNS--IAAMYQAVGELPOANRDTLAFIMHLOEVA--QSPHTKMDVANLAKVF 500
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 QILGITCVSSSLRVTCGQILRLSLPEHNYVTLRYLMGFLHANSRESIFNKMSSNLACVF 346
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 501 GPTIAHAVNPDPVTMGODIKRQKRVVERLLSLPLEYWSQPMVEQENIDPLHVIENS 560
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 GNLN-----IMPSQGVSSLSLV-----PLNMFTELLIEYEKI----- 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 561 ARSTPOTPIKVSLLGPVTTPEHQL-----KTPSSSSLSQSVRSTLTXT 606
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 -FSTPEAPG-----EHGLAPWEGSRAAPLOEAVPRTQATGLTKPT 420
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Search completed: February 1, 2005, 14:20:36
Job time : 42 secs

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 1, 2005, 13:57:16 ; Search time 202 Seconds

(without alignments)
1800.182 Million cell updates/sec

Title: US-09-881-736A-2

Perfect score: 3243

Sequence: 1 MDVTMLNVNLFQQLVRRVE.....SKSATNLGRQGNFFASPMUK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	2	Q9P2W2
2	3237	99.8	632	2	Q9H0H5
3	3230	99.6	632	2	Q9NMN2
4	2919	90.0	570	2	Q9P250
5	2781	85.8	628	2	Q9BZ74
6	2734	84.3	628	2	Q9NWM1
7	2497.5	77.0	629	2	Q6NRH9
8	2476.5	76.4	629	2	AAH70771
9	2476.5	76.4	629	2	Q6NVL1
10	2476.5	76.4	629	2	AAH67994
11	2462.5	75.9	629	2	Q7ZWM6
12	2173	67.0	654	2	Q6P3H8
13	2173	67.0	654	2	AAH63983
14	1205.5	37.2	612	2	Q6DFI1
15	1182	36.4	255	2	Q9H9L9
16	864	26.6	625	2	Q9N9Z9
17	862	26.6	625	2	Q9N9Z9
18	853	26.3	171	2	Q6P26
19	853	26.3	171	2	AAH24144
20	763.5	23.5	456	2	Q7PMW7
21	571.5	17.6	456	2	Q8MRH0
22	547.5	16.9	681	2	Q9XUS9
23	477	14.7	384	1	RG84_DROME
24	477	14.7	384	1	AAH68049
25	431	13.3	354	2	Q95VR1
26	348	10.7	1980	1	MY9B_RAT
27	339.5	10.5	459	2	Q7ZU76
28	339.5	10.5	2114	1	MY9B_MOUSE
29	336	10.4	459	2	Q7T0E5
30	329	10.1	334	1	CHIN_RAT
31	328	10.1	334	1	CHIN_MOUSE

32	328	10.1	334	2	BAC35853
33	327	10.1	334	2	Q8BWU6
34	326	10.1	1107	2	Q6DE55
35	323.5	10.0	2158	1	MY9B_HUMAN
36	322	9.9	289	2	Q6TBE0
37	322	9.9	289	2	CAG33145
38	322	9.9	459	1	CHIN_HUMAN
39	320	9.9	299	2	Q92153
40	315	9.7	1337	2	Q6PCS4
41	315	9.7	1337	2	AAH59184
42	310	9.6	459	2	Q7TON5
43	308	9.5	635	2	Q94466
44	305.5	9.4	1317	1	GAP_CAEEL
45	303.5	9.4	332	2	Q6GN15

ALIGNMENTS

RESULT 1	Q9P2W2	PRELIMINARY;	PRT;	632 AA.
ID	Q9P2W2			
AC	Q9P2W2			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	GTPase activating protein.			
GN	Name=MgcracGAP;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI	Taxid=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20435340; PubMed=10979956;			
RA	Kawashima T., Hirose K., Satoh T., Kaneko A., Ikeda Y., Kaziro Y.,			
RT	"MgcracGAP is involved in the control of growth and differentiation of			
RT	hematopoietic cells."			
RL	Blood 96:2116-2124(2000).			
DR	EMBL; AB030251; BAA90247.1; -.			
DR	PIR; D59430; D59430.			
DR	HSSP; Q98935; 1F7C.			
DR	Inact; Q9P2W2; -.			
DR	GO; GO:0005489; F:electron transporter activity; IEA.			
DR	GO; GO:0005506; F:electron transport; IEA.			
DR	GO; GO:0006118; F:electron transport; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	InterPro; IPR001450; 4Fe4S ferredoxin.			
DR	InterPro; IPR002219; DAG_Pe-bind.			
DR	InterPro; IPR000198; RhOGAP.			
DR	InterPro; IPR008936; Rho_GAP.			
DR	Pfam; PF00130; Cl_1; 1.			
DR	Pfam; PF00620; RhOGAP; 1.			
DR	PRINTS; PR00353; 4FE4SFRDOXIN.			
DR	SMART; SM00109; Cl_1.			
DR	SMART; SM00324; RhOGAP; 1.			
DR	PROSITE; PS00479; DAG_Pe_BIND_DOM_1; 1.			
DR	PROSITE; PS00081; DAG_Pe_BIND_DOM_2; 1.			
DR	PROSITE; PS00238; RhOGAP; 1.			
DR	SEQUENCE 632 AA; 7100 MW; BC2B75E5A8739E2B CRC64;			
QY	Query Match	100.0%;	Score 3243;	DB 2; Length 632;
QY	Best Local Similarity	100.0%;	Pred No. 1e-192;	
QY	Matches	632;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MDVTMLNVNLFQQLVRRVEILSEGNVOFIQLAKDFEDFRKKMORTDHELGRYKDLMLK 60		
QY	1	MDVTMLNVNLFQQLVRRVEILSEGNVOFIQLAKDFEDFRKKMORTDHELGRYKDLMLK 60		
QY	61	AETERSALDYKLGKRNQVDVEIKRQRAADCEKLERQIQLIRELMKDTSSISLSE 120		
QY	61	AETERSALDYKLGKRNQVDVEIKRQRAADCEKLERQIQLIRELMKDTSSISLSE 120		
QY	61	AETERSALDYKLGKRNQVDVEIKRQRAADCEKLERQIQLIRELMKDTSSISLSE 120		

QY 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSLVKTFKLKKR 180
DB 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSLVKTFKLKKR 180
QY 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIVAKTTVVPNDGPIEAVSTIETVP 240
DB 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIVAKTTVVPNDGPIEAVSTIETVP 240
QY 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
DB 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
QY 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSF 360
DB 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSF 360
QY 361 MIPSIIVHCVNEIEBQGLTETGLYRISGCDRTVKEIKKFKPLRVKTVPLLSKVDDIHAICS 420
DB 361 MIPSIIVHCVNEIEBQGLTETGLYRISGCDRTVKEIKKFKPLRVKTVPLLSKVDDIHAICS 420
QY 421 LKDFLRLNKEPLLFRNLRAFMFAEITDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 480
DB 421 LKDFLRLNKEPLLFRNLRAFMFAEITDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 480
QY 481 QKVAOSPHTKMDVYANLAKYFGPTIVAHVNPDPVTMSODIKRQKRVYERLLSLPLEYWS 540
DB 481 QKVAOSPHTKMDVYANLAKYFGPTIVAHVNPDPVTMSODIKRQKRVYERLLSLPLEYWS 540
QY 541 QPMNVEQENIDPLHVTIENSNAPSTPOTPIKVSILGCVTTPPEHQLKTPESSSSLSQVRVS 600
DB 541 QPMNVEQENIDPLHVTIENSNAPSTPOTPIKVSILGCVTTPPEHQLKTPESSSSLSQVRVS 600
QY 601 TLTKNTPRFGSKSKSATNLGRQGNFPASPMUK 632
DB 601 TLTKNTPRFGSKSKSATNLGRQGNFPASPMUK 632
RESULT 2
Q9H0H5 PRELIMINARY; PRT; 632 AA.
AC Q9H0H5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein DKFZp434C011 (RACGAP1 protein).
GN Name=DKFZp434C011; Synonyms=RACGAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Pousetka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stalcenon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Straubeberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Ebert U., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136794; CAB66728.1; -;
DR EMBL; BC032754; AAH32754.1; -;
DR EMBL; CR533565; CAG38596.1; -;
DR HSSP; Q98935; 1F7C.
DR Genew; HGNC:9804; RACGAP1.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; P:iron ion binding; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR GO; GO:007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR000198; RhGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; CL_1; 1._GAP.
DR Pfam; PF00620; RhGAP; 1.
DR PRINTS; PR00353; 4FE4SFERDOXIN.
DR SMART; SM00109; CL; 1.
DR SMART; SM00324; RhGAP; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS0238; RhGAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 632 AA; 71026 MW; 032B7D9F9CEA8F39D CRC64;
Query Match 99.8%; Score 3237; DB 2; Length 632;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDTMNLVNNLEFQIVRRVEILSEGENEVOFIQAKDFEDFRKKWORTDHEIKYDILMK 60
DB 1 MDTMNLVNNLEFQIVRRVEILSEGENEVOFIQAKDFEDFRKKWORTDHEIKYDILMK 60
QY 61 AETESALDVKLKHARNOVDVETIKRQRAEADCEKLERGIQLIREMLMCDTSGSIQLSSE 120
DB 61 AETESALDVKLKHARNOVDVETIKRQRAEADCEKLERGIQLIREMLMCDTSGSIQLSSE 120
QY 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSLVKTFKLKKR 180
DB 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSLVKTFKLKKR 180
QY 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIVAKTTVVPNDGPIEAVSTIETVP 240
DB 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIVAKTTVVPNDGPIEAVSTIETVP 240
QY 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
DB 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
QY 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSF 360
DB 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSF 360
QY 361 MIPSIIVHCVNEIEBQGLTETGLYRISGCDRTVKEIKKFKPLRVKTVPLLSKVDDIHAICS 420
DB 361 MIPSIIVHCVNEIEBQGLTETGLYRISGCDRTVKEIKKFKPLRVKTVPLLSKVDDIHAICS 420
QY 421 LKDFLRLNKEPLLFRNLRAFMFAEITDEDNSTIAAMYQAVGELPQANRDTLAFMLIH 480

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DB 421 LKDFLRNKEPLFLRLNRAFMFAEITDEDNSIAAMYQAVGELPOANDTLAFLMIH 480
QY 481 QRYAOSPHRTKMDVANIAXKFGPTIVAAHVPNDPVTMSODIKRQPKVERLLSLPLEYWS 540
DB 481 QRYAOSPHRTKMDVANIAXKFGPTIVAAHVPNDPVTMLDQIKRQPKVERLLSLPLEYWS 540
QY 541 QPMWVEQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQVRWS 600
DB 541 QPMWVEQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQVRWS 600
QY 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMLK 632

RESULT 3
Q9NMN2 PRELIMINARY; PRT; 632 AA.
ID Q9NMN2;
AC Q9NMN2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ20726.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obauchi M.,
RA Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isoqai T., Sugano S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000733; BAA91347.1; -.
DR HSP; Q98935; IFC.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002219; DAG_P8-bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR PRINTS; PR00353; 4F8SFRDOXIN.
DR SMART; SM00109; Cl_1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS00479; DAG_P8_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_P8_BIND_DOM_2; 1.
DR PROSITE; PS00238; RHO_GAP; 1.
SQ SEQUENCE 632 AA; 71048 MW; 7DC06CB725BBA44 CRC64;

Query Match 99.6%; Score 3230; DB 2; Length 632;
Best Local Similarity 99.7%; Pred. No. 6,5e-192;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIRPESC 300
DB 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIRPESC 300
QY 301 VPCGRKIKKGLSLKCRDRVNSHPBCRDRCPICPTLIGTPVKIGEGMLDFVSQTSR 360
DB 301 VPCGRKIKKGLSLKCRDRVNSHPBCRDRCPICPTLIGTPVKIGEGMLDFVSQTSR 360
QY 361 MFSIVHCVNEIEQGLTETGLYRISGCDRTVKEKEFLRKVPLLSKYDDIAICS 420
DB 361 MFSIVHCVNEIEQGLTETGLYRISGCDRTVKEKEFLRKVPLLSKYDDIAICS 420
QY 421 LKDFLRNKEPLFLRLNRAFMFAEITDEDNSIAAMYQAVGELPOANDTLAFLMIH 480
DB 421 LKDFLRNKEPLFLRLNRAFMFAEITDEDNSIAAMYQAVGELPOANDTLAFLMIH 480
QY 481 QRYAOSPHRTKMDVANIAXKFGPTIVAAHVPNDPVTMSODIKRQPKVERLLSLPLEYWS 540
DB 481 QRYAOSPHRTKMDVANIAXKFGPTIVAAHVPNDPVTMLDQIKRQPKVERLLSLPLEYWS 540
QY 541 QPMWVEQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQVRWS 600
DB 541 QPMWVEQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQVRWS 600
QY 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMLK 632

RESULT 4
Q9P250 PRELIMINARY; PRT; 570 AA.
ID Q9P250;
AC Q9P250;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA1478 protein (Fragment).
GN Name=KIAA1478;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Ref. 7,143-150 (2000).
DR EMBL; AB040911; BAA96002.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002219; DAG_P8-bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR PRINTS; PR00353; 4F8SFRDOXIN.
DR SMART; SM00109; Cl_1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS00479; DAG_P8_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_P8_BIND_DOM_2; 1.
DR PROSITE; PS00238; RHO_GAP; 1.
FT NON TER 1
SQ SEQUENCE 570 AA; 63468 MW; A03F36C0AA65485 CRC64;

Query Match 90.0%; Score 2919; DB 2; Length 570;
Best Local Similarity 99.8%; Pred. No. 1.1e-172;

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Matches 569, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 63 TERSALDVYLKARNQVDVEIKRORAEADCEKLEROIOLIREMLMCDTSGSIOLSEBK 122
 Db 1 TERSALDVYLKARNQVDVEIKRORAEADCEKLEROIOLIREMLMCDTSGSIOLSEBK 60
 QY 123 SALAFINRQGPSSSNAAGNRKLSITIDSGSILSDISFDKTDSELDMDSSIVKTPKLRK 182
 Db 61 SALAFINRQGPSSSNAAGNRKLSITIDSGSILSDISFDKTDSELDMDSSIVKTPKLRK 120
 QY 183 RSTSRQFVDGPPGPKYKTRISGSAVDQNESIVAKTIVTVPDGPIEAVSTIETVPW 242
 Db 121 RSTSRQFVDGPPGPKYKTRISGSAVDQNESIVAKTIVTVPDGPIEAVSTIETVPW 180
 QY 243 TRSRRTGTGLQPNNSDPTLNSRQLEBRTETDSVGTPOSGMRLHDFVSKTVIKPESQVP 302
 Db 181 TRSRRTGTGLQPNNSDPTLNSRQLEBRTETDSVGTPOSGMRLHDFVSKTVIKPESQVP 240
 QY 303 CGKRIKFGKLSLKCRDQVSVSHPECRDRCPLPILIGTPVKIGGMADFVSQTSPI 362
 Db 241 CGKRIKFGKLSLKCRDQVSVSHPECRDRCPLPILIGTPVKIGGMADFVSQTSPI 300
 QY 363 PSIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHALCSIL 422
 Db 301 PSIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHALCSIL 360
 QY 423 KQFLNLIKPELTLFRLNRAFEAEITDEBNSIAAMYQAVGELPOANRDTLAFIMHLOR 482
 Db 361 KQFLNLIKPELTLFRLNRAFEAEITDEBNSIAAMYQAVGELPOANRDTLAFIMHLOR 420
 QY 483 VAQSPHTKMDVANLAKVFGPTIVAAVNPDPVTMSQDIKROPKVERLLSLPLEYWSQF 542
 Db 421 VAQSPHTKMDVANLAKVFGPTIVAAVNPDPVTMLQDIKROPKVERLLSLPLEYWSQF 480
 QY 543 MNVBEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPHQLKTPSSSSLSQVRSL 602
 Db 481 MNVBEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPHQLKTPSSSSLSQVRSL 540
 QY 603 TKNTPRFGSKSATNLGRQGNFASPMLK 632
 Db 541 TKNTPRFGSKSATNLGRQGNFASPMLK 570

RESULT 5

Q9BZ74 PRELIMINARY; PRT; 628 AA.

AC Q9BZ74; 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
 DE FKSG42.
 GN Name=FKSG42;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang Y.-G., Gong L.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF34184; AAG50293.1; -;
 DR HSSP; Q98935; 1F7C.
 DR InterPro; IPR000198; RhogAP.
 DR InterPro; IPR008936; Rho GAP.
 DR Pfam; PF00620; RhogAP; 1.
 DR SMART; SM00324; RhogAP; 1.
 DR PROSITE; PS50238; RHOGAP; 1.
 SQ SEQUENCE 628 AA; 70013 MW; A142855A613154CC CRC64;

Query Match 85.8%; Score 2781; DB 2; Length 628;
 Best Local Similarity 87.0%; Pred. No. 4,6e-164;
 Matches 550; Conservative 31; Mismatches 47; Indels 4; Gaps 2;

QY 1 MDTMLNRLNFEQIVRVEILLSENGEVOFIOLADPFDFPKKQRTDHELAKYDLMK 60
 Db 1 MDTMLNRLNFEQIVRVEILLSENGEVOFIOLADPFDFPKKQRTDHELAKYDLMK 60
 QY 61 ATERSALDVYLKARNQVDVEIKRORAEADCEKLEROIOLIREMLMCDTSGSIOLSEBK 120
 Db 61 ATERSALDVYLKARNQVDVEIKRORAEADCEKLEROIOLIREMLMCDTSGSIOLSEBK 120
 QY 121 OKSALAFINRQGPSSSNAAGNRKLSITIDSGSILSDISFDKTDSELDMDSSIVKTPKLRK 180
 Db 121 OKSALAFINRQGPSSSNAAGNRKLSITIDSGSILSDISFDKTDSELDMDSSIVKTPKLRK 180
 QY 181 EKRSTSRQFVDGPPGPKYKTRISGSAVDQNESIVAKTIVTVPDGPIEAVSTIETVPW 240
 Db 181 EKRSTSRQFVDGPPGPKYKTRISGSAVDQNESIVAKTIVTVPDGPIEAVSTIETVPW 240
 QY 241 YWTRSRRTGTGLQPNNSDPTLNSRQLEBRTETDSVGTPOSGMRLHDFVSKTVIKPESQVP 300
 Db 241 YWTRSRRTGTGLQPNNSDPTLNSRQLEBRTETDSVGTPOSGMRLHDFVSKTVIKPESQVP 300
 QY 301 VPCGRRIKFGKLSLKCRDQVSVSHPECRDRCPLPILIGTPVKIGGMADFVSQTSPI 360
 Db 301 VPCGRRIKFGKLSLKCRDQVSVSHPECRDRCPLPILIGTPVKIGGMADFVSQTSPI 360
 QY 361 MIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHALCS 420
 Db 361 MIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHALCS 419
 QY 421 LKQDLNLIKPELTLFRLNRAFEAEITDEBNSIAAMYQAVGELPOANRDTLAFIMHLOR 480
 Db 420 LKQDLNLIKPELTLFRLNRAFEAEITDEBNSIAAMYQAVGELPOANRDTLAFIMHLOR 479
 QY 481 QPVAQSPHTKMDVANLAKVFGPTIVAAVNPDPVTMSQDIKROPKVERLLSLPLEYWSQF 540
 Db 480 QPVAQSPHTKMDVANLAKVFGPTIVAAVNPDPVTMLQDIKROPKVERLLSLPLEYWSQF 539
 QY 541 QPMVBEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPHQLKTPSSSSLSQVRSL 600
 Db 540 QPMVBEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPHQLKTPSSSSLSQVRSL 596
 QY 601 TLTNTPRFGSKSATNLGRQGNFASPMLK 632
 Db 597 TLTNTPRFGSKSATNLGRQGNFASPMLK 628

RESULT 6

Q9WVW1 PRELIMINARY; PRT; 628 AA.

AC Q9WVW1; 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, last annotation update)
 DE Rac GTPase-activating protein (MgcracGAP variant alpha) (MgcracGAP
 GN Name=Racgapi1; Synonym=MgcracGAP;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9249188; PubMed=10235109;
 RA Woolferton E.J., Halotis T., Mueller C.R.;
 RT "Identification and characterization of a transcript for a novel Rac
 RT GTPase-activating protein in terminally differentiating 3T3-L1
 RT adipocytes.";
 RL DNA Cell Biol. 18:265-273 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435340; PubMed=10979956;
 RA Kawashima T., Hirose K., Satoh T., Kaneko A., Ikeda Y., Kaziro Y.,
 RA Nosaka T., Kitamura T.;
 RT "MgcracGAP is involved in the control of growth and differentiation of

RT hematoepietic cells." ;
 RL Blood 96:2116-2124(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1;
 RX MEDLINE=21184103; PubMed=11287179;
 RA Van de Putte T., Zwijssen A., Lonnay O., Rybin V., Cozijnsen M.,
 RA Francis A., Baekelandt V., Kozak C.A., Zerial M., Huybreck D.;
 RT "Mice with a homozygous gene trap vector insertion in mcracgap die
 during pre-implantation development." ;
 RL Mech. Dev. 102:33-44(2001).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzyviński M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF079974; AAD040487.1; -;
 DR EMBL; AB030252; BAA90248.1; -;
 DR EMBL; AF212320; AAG43539.1; -;
 DR EMBL; AF212321; AAG43540.1; -;
 DR EMBL; BC010715; AAI10715.1; -;
 DR HSSP; Q89935; 1F7C;
 DR MGD; MG1349423; Racgap1.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR001450; 4Fe4Sferredoxin.
 DR InterPro; IPR002219; DAG_PE_bind.
 DR InterPro; IPR000198; RhOGAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF00130; Cl_1; 1.
 DR Pfam; PF00620; RhOGAP_1.
 DR PRINTS; PRO0353; 4FE4SFRDOXIN.
 DR SMART; SM00109; Cl_1.
 DR SMART; SM00324; RhOGAP_1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50238; RhOGAP_1.
 SO SEQUENCE 628 AA; 70158 MW; 8D1B9DEC3CE057BE CRC64;

Query Match 84.3%; Score 2734; DB 2; Length 628;
 Best Local Similarity 84.4%; Pred. No. 3.8e-161;
 Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3;

QY 1 MDTMNLNRLFLPOLVRRVITLSEGN-VQFIQLANDPFPKPKMOTDHLKQYDLM 59
 DB 1 MDTMNLNRLFLPOLVRRVITLSEGNIEFQVVDFFRRKKYORTNOLEKFDLL 60

QY 60 KAETERSALDVKIKHARNOVDVEIKRQREADCEKLEHQIQLIREMLMCTSGSIQLSE 119
 DB 61 KAETGRSALDVKIKHARNOVDVEIKRQREAECAKLEQOIQLIRIDLMCTSGSIQLSE 120
 QY 120 EOKSALAFNLRRGPPSSNAGNRLSTIDSGSLTSDISPKDDESLDMSLWKTFLTK 179
 DB 121 EOKSALAFNLRRGASSGHGANNLSTIDSGSLTSDISPKDDESLDMSLWKTFLTK 180
 QY 180 REKRSTSRQFVGGPPGPKVKTSGISAVDOGNESIVAKTVVVPNDGPIEAVSTIETV 239
 DB 181 REKRSTSRQFIDGPPGPKVKTSGISAVDOGNESIVAKTVVVPNDGPIEAVSTIETV 240
 QY 240 PYWTSRRKRTGLQPNNSDSTLNSQLBPTETDVSQVPSNGMRHLDFSVKTVIKPES 299
 DB 241 PSWTSRRKSGPLQPNNSDSTLNSQLBPTETDVSQVPSNGMRHLDFSVKTVIKPES 300
 QY 300 CVPCGRIRKRGKSLKCRDQVSHVSHCECDRCPLPCLITLGPVTVIGEMLADFPVSQTS 359
 DB 301 CVPCGRIRKRGKSLKCRDQVSHVSHCECDRCPLPCLITLGPVTVIGEMLADFPVSQTS 360
 QY 360 PMIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLKVTVPILSKYVDIHAIC 419
 DB 361 PMIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLKVTVPILSKYVDIHAIC 420
 QY 420 SLKDELRLNKEPLTLFRNLRAFEAEITDEDSIAAMYQAVGELPQANRDTLAFLMIH 479
 DB 421 SLKDELRLNKEPLTLFRNLRAFEAEITDEDSIAAMYQAVGELPQANRDTLAFLMIH 480
 QY 480 LQVAVSPHTKMDVNLAKVFGPTIYAHAVPNPDPTMSODIRGQKRVVERLLSLPLEYV 539
 DB 481 LQVAVSPHTKMDVNLAKVFGPTIYAHAVPNPDPTMSODIRGQKRVVERLLSLPLEYV 540
 QY 540 SCFMATVEOENIDPLAVIENSNAFSTPOTPDIKSLGPTVTPPHOHLKTPSSSLSORVR 599
 DB 541 SCFMATVEOENIDPLAVIENSNAFSTPOTPDIKSLGPTVTPPHOHLKTPSSSLSORVR 596
 QY 600 STLTNTNTPRFGSKSKSATNLGRQGNFASBMLK 632
 DB 597 N-LSKSTPRNGSKSATNLGGQKFFPAPYLK 628

RESULT 7
 ID 06NRH9 PRELIMINARY; PRT; 629 AA.
 AC 06NRH9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE MCC83804 protein.
 GN Name=MGC83804;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocytes; PubMed=12477932;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070771; AAH70771.1; -
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002219; DAG_P6-bind.
DR InterPro; IPR001198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR PRINTS; PR00353; 4Fe4S_FDXIN.
DR SMART; SM00109; Cl_1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS00479; DAG_P6_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_P6_BIND_DOM_2; 1.
DR PROSITE; PS50238; RHO_GAP; 1.
SQ SEQUENCE 629 AA; 70781 MW; 40BB97C1CBADFC2 CRC64;

Query Match 77.0%; Score 2497.5; DB 2; Length 629;
Best Local Similarity 76.1%; Pred. No. 1.8e-146;
Matches 482; Conservative 78; Mismatches 68; Indels 5; Gaps 4;

1 MDTMNLNRLNLEFQOLMRQVDGNEGIEPFIQLAKNFEDFRKKQSRTHDELGYKDLMLK 60
1 MATNMLNRLNLEFQOLMRQVDGNEGIEPFIQLAKNFEDFRKKQSRTHDELGYKDLMLK 60
61 AETESALDVKLKHANQVDVEIKRQRAEADCEKLERQIQIIREMLMCDTSGSISLSE 120
61 TETESALDVKLKHANQVDVEIKRQRAEADCEKLERQIQIIREMLMCDTSGSISLSE 120
121 QKSALAFI-NRQOPSSNAGNKRSLTIDSSGSLISIDSKTDESIDMSSILVKTFRKLK 179
121 QKSALAFI-NRQOPSSNAGNKRSLTIDSSGSLISIDSKTDESIDMSSILVKTFRKLK 179
180 REKRSTSRQFVDPGPPVKTSTSGSAVDQNGESTVAKTIVTVPRDGGPIEAVSTIEV 239
180 REKRSTSRQFVDPGPPVKTSTSGSAVDQNGESTVAKTIVTVPRDGGPIEAVSTIEV 239
240 PYWTSRRKRTGLQPNWSDSTNSRQLPRTETDSVGTPOSGNKLMDHFSVKTIVKPS 299
240 PYWTSRRKRTGLQPNWSDSTNSRQLPRTETDSVGTPOSGNKLMDHFSVKTIVKPS 299
240 PYWTSRRKRTGLQPNWSDSTNSRQLPRTETDSVGTPOSGNKLMDHFSVKTIVKPS 299
300 CYPCKGRIRFEKLSLKCRDRCRVASHCEGDRCPICPIPLIGTPVKIGGMLADPFSQTS 359
300 CYPCKGRIRFEKLSLKCRDRCRVASHCEGDRCPICPIPLIGTPVKIGGMLADPFSQTS 359
299 CYPCKGRIRFEKLSLKCRDRCRVASHCEGDRCPICPIPLIGTPVKIGGMLADPFSQTS 358
360 PMIPSTIVACNEIEORGLTEGLVYISGCDRTVKEKKEFKLRVKVPLSLSKVDIHAIC 419
360 PMIPSTIVACNEIEORGLTEGLVYISGCDRTVKEKKEFKLRVKVPLSLSKVDIHAIC 419
359 PMIPSTIVACNEIEORGLTEGLVYISGCDRTVKEKKEFKLRVKVPLSLSKVDIHAIC 418
420 SLIKDFLRNLKEPLILFRNLRAFMEEAAETIDEDNSIAAMYQAVGELPQANRDTLAFIMH 479
420 SLIKDFLRNLKEPLILFRNLRAFMEEAAETIDEDNSIAAMYQAVGELPQANRDTLAFIMH 479
419 GFLKDFLRNLKEPLILFRNLRAFMEEAAETIDEDNSIAAMYQAVGELPQANRDTLAFIMH 478
480 LORVQASPDCKMDVSNLAKVFCPTLVGHAVSPDPDPMTLIQDTRQPMVLERLSLPAEYW 538
480 LORVQASPDCKMDVSNLAKVFCPTLVGHAVSPDPDPMTLIQDTRQPMVLERLSLPAEYW 538

DB 479 LORVQASPDCKMDVSNLAKVFCPTLVGHAVSPDPDPMTLIQDTRQPMVLERLSLPAEYW 538
QY 540 SQPMWVEGENDPLHVIENSNAFSTPQTPIDIKVSLGPAVTPPEHQLKTPSSSSSQRVR 599
DB 539 NOYMYV--ENIDPNHIIENSNVFSTPQTPIDAVSNLGLPTTPEQFPNKTPSSSSVSQRWK 596
QY 600 STLTNTPRPFSGSKSATNLGROGNFASPMUK 632
DB 597 STISNTPWFSGSKSATNSIPROGNFASPMUK 629

RESULT 8
AAH70771 PRELIMINARY; PRT; 629 AA.

AC AAH70771;
DT 13-MAY-2004 (TREMBlrel. 27, Created)
DT 13-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 13-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCB|TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070771; AAH70771.1; -
DR EMBL; BC070771; AAH70771.1; -
KW Hypothetical protein.

SQ SEQUENCE 629 AA; 70781 MW; 40BB97C1CBADFC2 CRC64;

Query Match 77.0%; Score 2497.5; DB 2; Length 629;
Best Local Similarity 76.1%; Pred. No. 1.8e-146;
Matches 482; Conservative 78; Mismatches 68; Indels 5; Gaps 4;

1 MDTMNLNRLNLEFQOLMRQVDGNEGIEPFIQLAKNFEDFRKKQSRTHDELGYKDLMLK 60
1 MATNMLNRLNLEFQOLMRQVDGNEGIEPFIQLAKNFEDFRKKQSRTHDELGYKDLMLK 60

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QY 61 AETERSALDVKLKHANQVDVEIKRQRAEADCEKLEROIQILIRELMCDTSGSIQLSER 120
DB 61 TETERSALEVKLKHANQVDVEIKRQRAEADCEKLEROIQILIRELMCDPSSGSIQLSER 120
QY 121 QKSALAFI-NRQOPSSNAGNKRSLTIDSGSILSDISFDKDESDLDWSSLVKTRKLLK 179
DB 121 QKSALAFI-NRQOPSSNAGNKRSLTIDSGSILSDISFDKDESDLDWSSLVKTRKLLK 180
QY 180 REKRSTSRQFDPGPPVKTSTIGSAVDQNGESIIVAKTIVTPVNDGGPIEAVSTIET 239
DB 181 REKRSTSRQFDPGPPVKTSTIGSAVDQNGESIIVAKTIVTPVNDGGPIEAVSTIET 239
QY 240 PYWTSRRRTGTLQPNNSDSTINSRLQLEPRTETDSVGTPOSGNKLHDFVSKTVIKPES 299
DB 240 PYWTSRRRTGTLQPNNSDSTINSRLQLEPRTETDSVGTPOSGNKLHDFVSKTVIKPES 298
QY 300 CVPCKGRIFGKLSLKCRDQVAVSHPECDRCPLPCTIPLTIGTPVKIGEGMLADPVISQTS 359
DB 299 CVPCKGRIFGKLSLKCRDQVAVSHPECDRCPLPCTIPLTIGTPVKIGEGMLADPVISQTS 358
QY 360 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKKFPLVKTVPILSKVDIHAIC 419
DB 359 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKKFPLVKTVPILSKVDIHAIC 418
QY 420 SLIKDFLRNLKPEPLTFLRLNRAFMEEAEITDEDNSTIANYQAVGELPOANRDTLAFIMH 479
DB 419 GFLKDFLRNLKPEPLTFLRLNRAFMEEAEITDEDNSTIANYQAVGELPOANRDTLAFIMH 478
QY 480 LORVAVSPHTKQDVANLAVFPGPTIYAHAVPNPDVPTVMSODIKRQPKVVERLISPLEY 539
DB 479 LORVAVSPHTKQDVANLAVFPGPTIYAHAVPNPDVPTVMSODIKRQPKVVERLISPLEY 538
QY 540 SQPMWVEGNDIPLVHTEIENSNAFSTPOTDIXSLIGPVTTPHOLKTPSSSSISQRR 599
DB 539 SQPMWVEGNDIPLVHTEIENSNAFSTPOTDIXSLIGPVTTPHOLKTPSSSSISQRR 596
QY 600 STLTXTTPRFGSKSATNLGROGNFASPMK 632
DB 597 STLTXTTPRFGSKSATNLGROGNFASPMK 629

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyviński M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RL Klein S., Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067994; AA67994.1; -
DR InterPro; IPR001450; 4Fe4s_ferredoxin.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR SMART; SM00109; Cl_1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS0061; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50238; RHO_GAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 629 AA; 7111 MW; BF17EB8A3456077A CRC64;

Query Match 76.4%; Score 2476.5; DB 2; Length 629;
Best Local Similarity 75.5%; Pred. No. 3, 6e-145;
Matches 478; Conservative 77; Mismatches 73; Indels 5; Gaps 4;

QY 1 MPTMNLNVLNPEOLVRARVEILSEGNVOFILOAKDFEPRFKKQRTDHELGKYLK 60
DB 1 MATINLNKLNLEBOLKRVQDGLNIEGIEPOFILOAKDFEPRFKKQSEBOLIKKMK 60
QY 61 AETERSALDVKLKHANQVDVEIKRQRAEADCEKLEROIQILIRELMCDTSGSIQLSER 120
DB 61 TETERSALEVKLKHANQVDVEIKRQRAEADCEKLEROIQILIRELMCDPSSGSIQLSER 120
QY 121 QKSALAFI-NRQOPSSNAGNKRSLTIDSGSILSDISFDKDESDLDWSSLVKTRKLLK 179
DB 121 QKSALAFI-NRQOPSSNAGNKRSLTIDSGSILSDISFDKDESDLDWSSLVKTRKLLK 180
QY 180 REKRSTSRQFDPGPPVKTSTIGSAVDQNGESIIVAKTIVTPVNDGGPIEAVSTIET 239
DB 181 REKRSTSRQFDPGPPVKTSTIGSAVDQNGESIIVAKTIVTPVNDGGPIEAVSTIET 239
QY 240 PYWTSRRRTGTLQPNNSDSTINSRLQLEPRTETDSVGTPOSGNKLHDFVSKTVIKPES 299
DB 240 PYWTSRRRTGTLQPNNSDSTINSRLQLEPRTETDSVGTPOSGNKLHDFVSKTVIKPES 298
QY 300 CVPCKGRIFGKLSLKCRDQVAVSHPECDRCPLPCTIPLTIGTPVKIGEGMLADPVISQTS 359
DB 299 CVPCKGRIFGKLSLKCRDQVAVSHPECDRCPLPCTIPLTIGTPVKIGEGMLADPVISQTS 358
QY 360 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKKFPLVKTVPILSKVDIHAIC 419
DB 359 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKKFPLVKTVPILSKVDIHAIC 418
QY 420 SLIKDFLRNLKPEPLTFLRLNRAFMEEAEITDEDNSTIANYQAVGELPOANRDTLAFIMH 479
DB 419 GFLKDFLRNLKPEPLTFLRLNRAFMEEAEITDEDNSTIANYQAVGELPOANRDTLAFIMH 478
QY 480 LORVAVSPHTKQDVANLAVFPGPTIYAHAVPNPDVPTVMSODIKRQPKVVERLISPLEY 539
DB 479 LORVAVSPHTKQDVANLAVFPGPTIYAHAVPNPDVPTVMSODIKRQPKVVERLISPLEY 538
QY 540 SQPMWVEGNDIPLVHTEIENSNAFSTPOTDIXSLIGPVTTPHOLKTPSSSSISQRR 599
DB 539 SQPMWVEGNDIPLVHTEIENSNAFSTPOTDIXSLIGPVTTPHOLKTPSSSSISQRR 596
QY 600 STLTXTTPRFGSKSATNLGROGNFASPMK 632

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Db      121 EQRSLAFLNARSQNPANINTSRRLATIDESASIIISDYKTDSDLDWSSAIRTRIX 180
Qy      179 KREKRRSTSRQFVDPGPPGVKKTSGISAVDQGNESIVAKTTVTVPNDGPIEAVSTIET 238
Db      161 KRQKRRS-SRNTTEGPAAKRSRSGRSEKGNESIVAKTTVTVPADGGPIEAVTVVA 239
Qy      239 VPYWTRSRKRT-----GTLOPNMSDSTLNSROLE-----PRTEDS-VG 276
Db      240 VPYWTRSRKRTVFCSSSEQCISINYSAAVEMDTVDSDVSQMDVFKQPSLPNAENRAPS 299
Qy      277 TPQSGKRLHDFVSCVTIVKPPESCVPQCGRIKFGKLSKCRQCRVAVSHCEGRDCLPCI 336
Db      300 TPQSGKRLHDFVSCVTIVKPPESCVPQCGRIKFGKLSKCRQCRVAVSHCEGRDCLPCI 359
Qy      337 PTLIGTPVKIGEGMLADPVFSQTSQPMIPSIIVHCVNEIEQRLTEGLYRISGCDRTVKEL 396
Db      360 PSMGTGTPVKIGEGMLADPVFSQTSQPMIPSIIVHCVNEIEQRLTEGLYRISGCDRTVKEL 419
Qy      397 KEKPLRKVTVPPLLSKYVDIHAICSLIKDPLRLKEPLTFRLNRAFMWAETDEDNSTIA 456
Db      420 KEKPLRKGTVPPLLSKYVEDIHAITGLIKDPLRLKEPLTFRLNRAFMWAETDEDNSTIA 479
Qy      457 ANYQAVGELPQANRDTLAFIMHLOQVVAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVT 516
Db      480 LMYQNIISDLPQHRDTLAFILHLOQVVAOSPHTKMDITNLARFGPTIVGHAVSNPEPMT 539
Qy      517 MSQDIKROPKVERRLISLPLEYWSQPMVVEQENIDPLH-VIENSNAFSTPQTDIKVSL 575
Db      540 IIQDTRKQPRVVERRLISLPLEYWSQPMIDHDHARDHMIENAVHT---TPDQMSMF 596
Qy      576 GCVTTPEHOLLTPSSSSLSQVR-SLTTKTPRGSKSKSATNLGROGNFPASPMLK 632
Db      597 GIIPTPDQMSKTPSSSSLSQRMKATLNAITPKFSSRSRAVAAVPRQGNFPASPMLK 654

RESULT 13
AAH63983 PRELIMINARY; PRT; 654 AA.
AC AAH63983;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein racgap1.
GN RACGAP1.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Whole;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins S.F., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Musina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullanb S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Kodrigues S., Sanchez A.,
RA Whiting M., Maan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN      [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC063983; AAH63983.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 654 AA; 73198 MW; CB656C1758B86DD8 CRC64;

Query Match      67.0%; Score 2173; DB 2; Length 654;
Best Local Similarity 64.6%; Pred. No. 2,5e-126;
Matches 425; Conservative 104; Mismatches 99; Indels 30; Gaps 9;

Qy      1 MDTMLANRNLEQOLVRVEIISSEGEVQIOLADFEDEFKKNQRTDHELCKYDLMK 60
Db      1 METAVNHNHSIFESIRADADVINESIEPQIOLANFENRRRMRLBELNACKCEVLTK 60
Qy      61 AETRSALDYKIKHARNVDVETIKRORAEADCEKLEPQIOLIREMLMD-NGSIOISE 119
Db      61 AETRGALAEVKKHARNVDVETIRROKASECAKDLQILRELVSESSSITQIME 120
Qy      120 EQRSLAFLN-RQPSNNAGNKRSLTIDESGSIISDIFSFKTDESLDWSSLVKTFKLK 178
Db      121 EQRSLAFLNARSQNPANINTSRRLATIDESASIIISDYKTDSDLDWSSAIRTRIX 180
Qy      179 KREKRRSTSRQFVDPGPPGVKKTSGISAVDQGNESIVAKTTVTVPNDGPIEAVSTIET 238
Db      181 KRQKRRS-SRNTTEGPAAKRSRSGRSEKGNESIVAKTTVTVPADGGPIEAVTVVA 239
Qy      239 VPYWTRSRKRT-----GTLOPNMSDSTLNSROLE-----PRTEDS-VG 276
Db      240 VPYWTRSRKRTVFCSSSEQCISINYSAAVEMDTVDSDVSQMDVFKQPSLPNAENRAPS 299
Qy      277 TPQSGKRLHDFVSCVTIVKPPESCVPQCGRIKFGKLSKCRQCRVAVSHCEGRDCLPCI 336
Db      300 TPQSGKRLHDFVSCVTIVKPPESCVPQCGRIKFGKLSKCRQCRVAVSHCEGRDCLPCI 359
Qy      337 PTLIGTPVKIGEGMLADPVFSQTSQPMIPSIIVHCVNEIEQRLTEGLYRISGCDRTVKEL 396
Db      360 PSMGTGTPVKIGEGMLADPVFSQTSQPMIPSIIVHCVNEIEQRLTEGLYRISGCDRTVKEL 419
Qy      397 KEKPLRKVTVPPLLSKYVDIHAICSLIKDPLRLKEPLTFRLNRAFMWAETDEDNSTIA 456
Db      420 KEKPLRKGTVPPLLSKYVEDIHAITGLIKDPLRLKEPLTFRLNRAFMWAETDEDNSTIA 479
Qy      457 ANYQAVGELPQANRDTLAFIMHLOQVVAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVT 516
Db      480 LMYQNIISDLPQHRDTLAFILHLOQVVAOSPHTKMDITNLARFGPTIVGHAVSNPEPMT 539
Qy      517 MSQDIKROPKVERRLISLPLEYWSQPMVVEQENIDPLH-VIENSNAFSTPQTDIKVSL 575
Db      540 IIQDTRKQPRVVERRLISLPLEYWSQPMIDHDHARDHMIENAVHT---TPDQMSMF 596
Qy      576 GCVTTPEHOLLTPSSSSLSQVR-SLTTKTPRGSKSKSATNLGROGNFPASPMLK 632
Db      597 GIIPTPDQMSKTPSSSSLSQRMKATLNAITPKFSSRSRAVAAVPRQGNFPASPMLK 654

RESULT 14
AAH63983 PRELIMINARY; PRT; 612 AA.
AC AAH63983;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
OX [1]
RN SEQUENCE FROM N.A.

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RC TISSUE-Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschuler R.D., Collins F.S., Wagner L., Shmolen C.M., Schuler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lomeliello N.A., Peters G.J., Abramson R.D., Millaby S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalobos S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Huily S.W.,
 RA Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX Klein S., Strausberg R.,
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC076756; AAH76756.1;
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 612 AA; 68707 MW; 63CB6C63EDD39308 CRC64;

Query Match 37.2%; Score 1205.5; DB 2; Length 612;
 Best Local Similarity 41.5%; Pred. No. 2,4e-66;
 Matches 268; Conservative 109; Mismatches 206; Indels 63; Gaps 15;

2 DTMMLNVRNLFEDVAVRVEILSGENVQFIQLAKDEDPFKKQORDHEIGKTKDLIMKA 61
 10 DTRKKVQLQSYLDRIILKIFIR-FNVSADDEFIQVARSFETSRKRQOHVEQLRDRKRETLVKC 68
 62. ETERSLADVYLKHARQOVDEIKRRORAEADCEKLEKROILIREMLMCDTSGSISQISEEQ 121
 69 ETERSLADVYLKHARQOVDEIKRRORAEADCEKLEKROILIREMLMCDTSGSISQISEEQ 126
 122 KSALAFINLNGQPS--SNAGNKLSTIDES--GSILSDISFDKTDSELDWDSLVKTFKTK 178
 127 -SVLAFVGGSRVSTPQAGKSRSLVYDESCFSLSDISYDTHREDDLDDELGGKPKVK 185
 179 KKRKRSTSRQFDGPPGPKYK---TRISGSAVDGNEISVAKTYTTVVNDGSPLEAVS 234
 186 ARRRRSSSLAPL-----APLKRPRSEAAIYAENVREIVINTVLV-TDAGPIHAIS 240
 235 TIEIVPYMTRSRK-----TGTLPNNSDSTLNSRLEPRTETSDVGTQSNQGR 285
 241 TIEAVR-RRSRKRAISSIQDHTSVLPQINED-----EKMEBEMPNHPKP-----TR 290
 286 LHDVFAKTVIKPSCVPCQKRIKFKSLKCRDQVAVSHPECRDCEPLPTL--IGTP 343
 291 THVYLSRTMIRAVCVCCQKVFQKCKXCKDRIILHECKDPCFKVSSSTFPSSGTI 350
 344 VKIGEMLADPVQSTSPMISIVHVCNEIEQGLTETGLYRISGCDRTYKELKELRV 403
 351 LKNGPVLADPAPMPRPVSLVIOCVNEIEKRLRERGIYIRPGCDRLVKELEPKLLQG 410

QY 404 KTVPLLSKVDIHAICSLKDKPLRNKEPLIFRLNRAPEMAEATDEEDNSIAATQAVG 463
 DB 411 KIRAGHAKEDHITVGCALKEFRRLQEPFLTSYLAFTLADADIIDECGGRATCOAVH 470
 QY 464 ELPOARNDTLAPLMIHQRVAGSPHTKMDVANLAKFGPIYAHAPNDPVTMSQDIR 523
 DB 471 DLPAERDITLAPLILHLYVMOSSECKMDKTNLIRFGLPLVGYSPNBPPLMIDTPR 530
 QY 524 QPKVRELSLPLEYMSQFMVMEQENIDPLHVIENSNAPSTPQTPDIKYSILGPVTPPEH 583
 DB 531 QAKVMSLISIPRFNMGFLFTQENKDSAKLDE-----RLFRPLTSPF- 575
 QY 584 QLLKTPSSSSLSQVRVSTFTKTPNPFSGSKSATNIGRQGNFASP 629
 DB 576 --INSASS-----LLKTPPLAQASAKSDLPKKAGRFPTSP 610

RESULT 15
 ID Q9H9L9 PRELIMINARY; PRT; 255 AA.
 AC Q9H9L9;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DE Hypothetical protein FLJ12664.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14702039;
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Iishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Mitsuhashi K., Yuki H., Oshima H., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsumawa H., Ichihara T., Shichida N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Sasaki H.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujikawa T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Okumori Y., Okamoto S.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Senba T.,
 RA Ohtsuki R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL: AK022726; BAB14206.1; -
 DR HSP; Q98935; I7C;
 DR InterPro: IPR000198; RhOGAP.
 DR InterPro: IPR008936; Rho GAP.
 DR Pfam: PF00620; RhOGAP; 1.
 DR SMART: SM00324; RhOGAP; 1.
 DR PROSITE: PSS0238; RhOGAP; 1.
 SQ SEQUENCE 255 AA; 28488 MW; B59D7B59385821BD CRC64;

Query Match 36.4%; Score 1182; DB 2; Length 255;

Best Local Similarity	99.2%;	Pred. No. 2e-65;	
Matches 234;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	397	KEKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLTFRLNRAFMEAAEITDEDSIA	456
Db	20	KLKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLTFRLNRAFMEAAEITDEDSIA	79
Qy	457	AMYQAVGELPQANRDTLAFMLHLOQVAAQSPHTKMDVANLAKYFGPTIVAHAVPNDPVT	516
Db	80	AMYQAVGELPQANRDTLAFMLHLOQVAAQSPHTKMDVANLAKYFGPTIVAHAVPNDPVT	139
Qy	517	MSODIKROPKVVVERLISLPLEYWSQFMVBOENIDPLHVIENSNAFSTPOTPDIKVSLG	576
Db	140	MLQDIKROPKVVVERLISLPLEYWSQFMVBOENIDPLHVIENSNAFSTPOTPDIKVSLG	199
Qy	577	PVTTPEHQLLKTSSSSSLSQRVSTLTKNTPRFGSKSKSATNLGROGNFFASPMLK	632
Db	200	PVTTPEHQLLKTSSSSSLSQRVSTLTKNTPRFGSKSKSATNLGROGNFFASPMLK	255

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